

5633076

APPROVED	O.G. FIG.	—
CLASS	SUBCLASS	
435 / 72.3		
BY	DRAFTSMAN	

sau96I

haeIII

asul

sau96I

nlaIV

hgIJII

ecoD109I

bsp1286

banII

asul

nlaIV

mnII  
mboII

aval apal mnII  
mnII ecoD109I

tth111I

1 GGA CTT GTC TTC CTC GTC CTG CTG TTC CTC GGG GCC CTC GGA CTG  
-18 Gly Leu Val Phe Leu Val Leu Leu Phe Leu Gly Ala Leu Gly Leu

haeIII  
eaeI  
cfrI

hInPI  
hhaI

46 TGT CTG GCT GGC CGT AGG AGA AGG AGT GTT CAG TGG TGC GCC GTA TCC  
-3 Cys Leu Ala Gly Arg Arg Arg Ser Val Gln Trp Cys Ala Val Ser

haeIII  
mnII  
aval haeI

94 CAA CCC GAG GCC ACA AAA TGC TTC CAA TGG CAA AGG AAT ATG AGA AAA  
14 Gln Pro Glu Ala Thr Lys Cys Phe Gln Trp Gln Arg Asn Met Arg Lys

mnII fnu4HI  
sau96I bbvI pleI  
haeIII alul hinfI bsrI  
asul pvuII bsmAI fokI  
142 GTG CTG GGC CCT CCT GTC AGC TGC ATA AAG AGA GAC TCC CCC ATC CAG  
30 Val Arg Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln

haeIII  
haeI  
scrFI haeIII  
ecoRII sau96I  
bstNI asul sfaNI

190 TGT ATC CAG GCC ATT GCG GAA AAC AGG GCC GAT GCT GTG ACC CTT GAT  
46 Cys Ile Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp

sau96I  
nlaIV  
scrFI  
ecoRII  
bstNI  
haeIII  
stul haeIII  
mnII haeI asul

238 GGT GGT TTC ATA TAC GAG GCA GGC CTG GCC CCC TAC AAA CTG CGA CCT  
62 Gly Gly Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro

FIG.-1A

sau96I  
 avail  
 asuI  
 fnu4HI accl nlaIV  
 286 GTA GCG GCG GAA GTC TAC GGG ACC GAA AGA CAG CCA CGA ACT CAC TAT  
 78 Val Ala Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr

fnu4HI  
 mboII bbvI aluI  
 hphI fnu4HI aluI pvuII  
 334 TAT GCC GTG GCT GTG GTG AAG AAG GGC GGC AGC TTT CAG CTG AAC GAA  
 94 Tyr Ala Val Ala Val Lys Lys Gly Ser Phe Gln Leu Asn Glu

haeIII sau96I  
 stuI avail  
 bglI haeI asuI fokI  
 382 CTG CAA GGT CTG AAG TCC TGC CAC ACA GGC CTT CGC AGG ACC GCT GGA  
 110 Leu Gln Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly

sau96I  
 avail  
 asuI  
 nlaIV  
 430 TGG AAT GTC CCT ACA GGG ACA CTT CGT CCA TTC TTG AAT TGG ACG GGT  
 126 Trp Asn Val Pro Thr Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly

hglJII aluI  
 bsp1286 fnu4HI  
 banII bbvI ddeI aluI  
 ddeI mnII pvuII mboII pvuII  
 478 CCA CCT GAG CCC ATT GAG GCA GCT GTG CAG TTC TTC TCA GCC AGC TGT  
 142 Pro Pro Glu Pro Ile Glu Ala Ala Val Gln Phe Phe Ser Ala Ser Cys

mspI  
 hpaII  
 scrFI  
 nciI  
 cauII  
 526 GTT CCC GGT GCA GAT AAA GGA CAG TTC CCC AAC CTG TGT CGC CTG TGT  
 158 Val Pro Gln Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys

nlaIV  
 scrFI  
 ecoRII  
 mnII bstNI rsal  
 574 GCG GGG ACA GGG GAA AAC AAA TGT GCC TTC TCC TCC CAG GAA CCG TAC  
 174 Ala Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr

FIG.-1B

APPROVED	O.G. FIG.
CLASS	SUBCLASS
BY	DRAFTSMAN

APPROVED	O.G. FIG.
CLASS	SUBCLASS
BY	DRAFTSMAN

nlaIV  
 hgiCI  
 aluI banI ddeI bsmal bsmal  
 622 TTC AGC TAC TCT GGT GCC TTC AAG TGT CTG AGA GAC GGG GCT GGA GAC  
 190 Phe Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp

sau96I  
 avall  
 asuI  
 ppuMI  
 hgiAI eco0109I  
 bsp1286 mnII mnII  
 670 GTG GCT TTT ATC AGA GAG AGC ACA GTG TTT GAG GAC CTG TCA GAC GAG  
 206 Val Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu  
 718 GCT GAA AGG GAC GAG TAT GAG TTA CTC TGC CCA GAC AAC ACT CGG AAG  
 222 Ala Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys

scrFI  
 ncII  
 mspl  
 hpaII  
 cauII  
 xmaI sau96I  
 smaI nlaIV  
 scrFI  
 ncII avall  
 cauII  
 aval asuI  
 sau96I ppuMI  
 haeIII nlaIV  
 asuI eco0109I nlaIII  
 bsrI  
 766 CCA GTG GAC AAG TTC AAA GAC TGC CAT CTG GCC CGG GTC CCT TCT CAT  
 238 Pro Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His

sfaNI  
 bglI draIII fokI mbolI  
 mnII hinFI  
 814 GCC GTT GTG GCA CGA AGT GTG AAT GGC AAG GAG GAT GCC ATC TGG AAT  
 254 Ala Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn  
 scrFI  
 ecoRII  
 bstNI hphI  
 862 CTT CTC CGC CAG GCA CAG GAA AAG TTT GGA AAG GAC AAG TCA CCG AAA  
 270 Leu Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys

FIG.-1C

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

sau3AI  
 mboI  
 dpnI  
 xholI  
 bstYI  
 bglII  
 aluI  
 bstXI nlaIV  
 910 TTC CAG CTC TTT GGC TCC CCT AGT GGG CAG AAA GAT CTG CTG TTC AAG  
 286 Phe Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys

nlaIV  
 hgiCI  
 pleI mnII bsp1286 mnII  
 hinfI taqI banI aval hinfI  
 958 GAC TCT GCC ATT GGG TTT TCG AGG GTG CCC CCG AGG ATA GAT TCT GGG  
 302 Asp Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly

mspI  
 styI hpall  
 rsal nlaIV fokI mnII  
 1006 CTG TAC CTT GGC TCC GGC TAC TTC ACT GCC ATC CAG AAC TTG AGG AAA  
 318 Leu Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys

mspI  
 hpall thal  
 scrFI fnuDII  
 nciI bstUI  
 mnII fnu4HI hinPI mnII  
 mnII bbyI cauI hhaI  
 1054 AGT GAG GAG GAA GTG GCT GCC CGG CGT GCG CGG GTC GTG TGG TGT GCG  
 344 Ser Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala

hinPI  
 mstI  
 fspI  
 fnu4HI  
 aluI hhaI bstXI  
 alwNI bbyI bsri  
 1102 GTG GGC GAG CAG GAG CTG CGC AAG TGT AAC CAG TGG AGT GGC TTG AGC  
 350 Val Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser

fnu4HI mnII  
 bbyI bspMI mnII haelliI mnII sfaNI  
 1150 GAA GGC AGC GTG ACC TGC TCC TCG GCC TCC ACC ACA GAG GAC TGC ATC  
 366 Glu Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile

scrFI  
 ecoRII bstXI  
 bstNI aluI sfaNI nlaIII fokI mnII  
 1198 GCC CTG GTG CTG AAA GGA GAA GCT GAT GCC ATG AGT TTG GAT GGA GGA  
 382 Ala Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly

**FIG.-1D**

APPROVED	O.G. FIG.	CLASS	SUBCLASS
		BY	
			DRAFTSMAN

n[allI	n[alIV	scrFI
sphI	hgiCI	ecoRII
rsal	nspCIx	bstNI
1246	TAT GTG TAC ACT GCA TGC AAA TGT GGT TTG GTG CCT GTC CTG GCA GAG	
398	Tyr Val Tyr Thr Ala Cys Lys Cys Gly Leu Val Pro Val Leu Ala Glu	

1294 AAC TAC AAA TCC CAA CAA AGC AGT GAC CCT GAT CCT AAC TGT GTG GAT 414 Asn Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp	<i>sau3AI</i> <i>mbol</i> <i>dpnI</i> <i>alwI</i>
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sau3AI	mboI
dpnI	
ecoNI	ecoRV
1342	AGA CCT GTG GAA GGA TAT CTT GCT GTG GCG GTG GTT AGG AGA TCA GAC
430	Arg Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp

scrFI  
ecoRII  
bstNI  
1390 ACT AGC CTT ACC TGG AAC TCT GTG AAA GGC AAG AAG TCC TGC CAC ACC  
446 Thr Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr

1438 GCC GTG GAC AGG ACT GCA GGC TGG AAT ATC CCC ATG GGC CTG CTC TTC 462 Ala Val Asp Arg Thr Ala Gly TrP Asn Ile Pro Met Gly Leu Leu Phe	<i>pstI</i> <i>haeIII</i> <i>nlaIII</i> <i>styI</i> <i>sau96I</i> <i>ncoI</i> <i>asul</i> <i>earI</i>	<i>mboll</i>
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	sau3AI															
	mbol															
	DpnI															
scrFI	xbaII															
ecoRII	bstYI	hgAI														
bstNI	avaI	bgI	bsp1286													
1534	GCC	CCT	GGG	TCT	GAC	CCG	AGA	TCT	AAT	CTC	TGT	GCT	CTG	TGT	ATT	GGC
484	Ala	Pro	Gly	Ser	Asp	Pro	Arg	Ser	Asn	Leu	Cys	Ala	Leu	Cys	Ile	Gly

## FIG.-1E

APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

1582 GAC GAG CAG GGT GAG AAT AAG TGC GTG CCC AAC AGC AAT GAG AGA TAC  
 510 Asp Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr

nlaIV  
 hgICl  
 banI scrFI  
 mspI ecoRII  
 bsrI hpaII bstNI ddeI bsmI bsmal  
 1630 TAC GGC TAC ACT GGG GCT TTC CGG TGC CTG GCT GAG AAT GCT GGA GAC  
 526 Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp  
 1678 GTT GCA TTT GTG AAA GAT GTC ACT GTC TTG CAG AAC ACT GAT GGA AAT  
 542 Val Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn

fnu4HI  
 bbvI  
 hlnPI  
 hhAI  
 mnI nlaIII ddeI aluI mnI  
 1726 AAC AAT GAG GCA TGG GCT AAG GAT TTG AAG CTG GCA GAC TTT GCG CTG  
 558 Asn Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu  
 taqI mnI  
 bglI mnI ddeI aluI fnu4HI  
 1774 CTG TGC CTC GAT GGC AAA CGG AAG CCT GTG ACT GAG GCT AGA AGC TGC  
 574 Leu Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys

sau96I  
 nlaIV  
 nlaIII  
 styI haeIII  
 ncoI asuI hinfl nlaIII bsmal fokI  
 1822 CAT CTT GCC ATG GCC CCG AAT CAT GCC GTG GTG TCT CGG ATG GAT AAG  
 590 His Leu Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys

fnu4HI  
 ecoNI alwNI bbvI  
 1870 GTG GAA CGC CTG AAA CAG GTG CTG CTC CAC CAA CAG GCT AAA TTT GGG  
 606 Val Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly

sau3AI  
 mboI mspI  
 dpnI hpaII  
 xbaII scrFI  
 bstYI nciI  
 alwI cauII bsrI  
 1919 AGA AAT GGA TCT GAC TGC CCG GAC AAG TTT TGC TTA TTC CAG TCT GAA  
 622 Arg Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu

FIG.-1F

APPROVED	O.G. FIG.
CLASS	SUBCLASS
BY	DRAFTSMAN

1966 ACC AAA AAC CTT CTG TTC AAT GAC AAC ACT GAG TGT CTG GCC AGA CTC  
 638 Thr Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu  
  
 sau96I  
 avall  
 asuI  
 nlaIII ndeI sspI nlaIV  
 2014 CAT GGC AAA ACA ACA TAT GAA AAA TAT TTG GGA CCA CAG TAT GTC GCA  
 654 His Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala  
  
 scrFI  
 ecoRII  
 hgIAI bstNI  
 bsp1286 mnI mnI  
 2062 GGC ATT ACT AAT CGT AAA AAG TGC TCA ACC TCC CCC CTC CTG GAA GCC  
 670 Gly Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala  
  
 ddeI  
 mstII  
 mnI  
 eco8II  
 ecoRI bsu36I  
 2110 TGT GAA TTC CTC AGG AAG TAA AACCGAAGAA GATGGCCCAG CTCCCCAAGA  
 685 Cys Glu Phe Leu Arg Lys DC\*  
  
 styI  
 haeIII  
 sau96I  
 mboII scrFI asuI  
 earI ecoRII nlaIV  
 aluI bstNI ecoD109I nlaIV  
 2161 AAGCCTCAGC CATTCACTGC CCCCCAGCTCT TCTCCCCAGG TGTGTTGGGG CCTTGGCTCC  
  
 ecoNI fokI ddeI  
 2221 CCTGCTGAAG GTGGGGATTG CCCATCCATC TGCTTACAAT TCCCTGCTGT CGTCTTAGCA  
  
 2281 AGAAGTAAAA TGAGAAATT TGTTGATATT CAAAAAAA  
  
 >LENGTH: 2319

FIG.-1G

APPROVED BY	O.G.	FIG.
	CLASS	SUBCLASS
DRAFTSMAN		

1	GACTCTAGG	GGCTTGAGA CCTAGTGGGA GAGAAAGAAC ATCGCAGCAG CCAGGACAGG TGAAGTGCAG GCTCTGCAGC
101	GGGGTTGGA	GTCTGTCTCT GCTCTAGGGC TTTCTAGGGC CTCAGTCCTC AAGGAACAGG TAGACCTGGC CGCGGGGAGT GGGGGGGAA GGGGGTGTCTA
201	TTGGCAACA	GGGGGAAA GGGCTGAATA AAGGGGCCA GGGGAGGCC AGTGTGGAGG CCTTCGTTTG CAAAGTCGCC TCCAGACCC AGAC ATG AAA CTT
-19		
304	GTC	TTC CTC GTC CTC CTC GGG GCC CTC GGA CTC GCT GGT CTG GCT GGT AGG AGG AGT GTT CAG TGG GCC GTA TCC
-16	V	F L V L L F L G A L G L C L A G R R S V Q W C A V S
391	CAA	CCC GAG GCC ACA AAA TGC TTC CAA TGG CAA AGG AAT ATG AGA AAA GTG CGT GGC CCT GTC AGC TGC ATA AAG AGA GAC TCC
14	Q	P E A T K C F Q W R N M R K V R G P V S C 1 K R D S
478	CCC	ATC CAG TGT ATC CAG GCC ATT GCG GAA AAC AGG GCG GAT GCT GTG ACC CTT GAT GGT TTC ATA TAC GAG GCA GGC CTG GCC
43	P	1 Q C 1 Q A 1 A E N R A D A V T L D G F 1 Y E A G L A
565	CCC	TAC AAA CTG CGA CCT GTC GCG GAA GTC TAC GGG ACC GAA AGA CAG CCA CGA ACT CAC TAT TAT GCC GTG GCT GTG GTG AAG
72	P	Y K L R P V A A E V Y G T E R Q P R T H Y Y A V A V V K
652	AAG	GGC GGC AGC TTT CAG CTG AAC GAA CTG CAA GGT CTG AAG TCC TGC CAC ACA GGC CTT CGC AGG ACC GCT GGA TGG AAT GTC CCT
101	K	G G S F Q L N E L Q G L K S C H T G L R R T A G W N V P
739	ACA	GGG ACA CTT CGT CCA TTC TGG AAT TGG ACC GGT CCA CCT GAG CCC ATT GAG GCA GCT GTG GCC AGG TTC TTC TCA GCC AGC TGT
130	T	G T L R P F L N W T G P P E P 1 E A A V A R F F S A S C
826	GTT	CCC GGT GCA GAT AAA GGA CAG TTC CCC AAC CTG TGT CGC CTG TGT GCG GGG ACA GGG GAA AAC AAA TGT GCC TTC TCC CAG
159	V	P G A D K G Q F P N L C R L C A G T G E N K C A F S S Q
913	GAA	CCG TAC TTC AGC TAC TCT GGT GCC TTC AAG TGT CTG AGA GAC GGG GCT GGA GAC GTG GCT TTT ATC AGA GAG AGC ACA GTG TTT
188	E	P Y F S Y S G A F K C L R D G A G D V A F I R E S T V F
1000	GAG	GAC CTG TCA GAC GAG GCT GAA AGG GAC GAG TAT GAG TTA CTC TGC CCA GAC AAC ACT CGG AAG CCA GTG GAC AAG TTC AAA GAC
217	E	D L S D E A E R D E Y E L L C P D N T R K P V D K F K D
1087	TGC	CAT CTG GCC CGG GTC CCT TCT CAT GCC GTT GTG GCA CGA AGT GTG AAT GGC AAG GAG GAT GCC ATC TGG AAT CTT CTC CGC CAG
246	C	H L A R V P S H A V A R S V N G K E D A 1 W N L L R Q
11174	GCA	CAG GAA AAG TTT GGA AAG GAC AAG TCA CCG AAA TTC CAG CTC TTT GGC TCC CCT AGT GGG CAG AAA GAT CTG CTG TTC AAG GAC
275	A	Q E K F G K D K S P K F Q L F G S P S G K D L F K D
11261	TCT	GCC ATT GGG TTT TCG AGG GTG CCC CCG AGG ATA GAT TCT GGG CTC TAC CTT GGC TCC GTC ACT GCC ATC CAG AAC TTG
304	S	A 1 G F S R V P R 1 D S G L Y L G S G Y F T A 1 Q N L
1348	AGG	AAA AGT GAG GAG GAA GTG GCT GCG CGG CGT GTC GTG TGG TGT GCG CGG GAG CAG GAG CTG CGC AAG TGT AAC AAC CAG
333	R	K S E E V A A R R A R V V C A R V V C A V G E Q E L R Q C

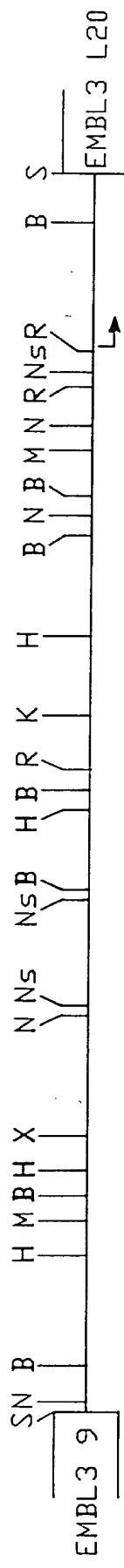
FIG. - 2 A

APPROVED	O.G. FIG.
BY	CLASS
	SUBCLASS
	DRAFTSMAN

1435 TGG AGT GGC TTG AGC GAA GGC ACC GTG TCC ACC ACA GAG GAC TGC ATC GCC CTG GTG CTG AAA GGA GAA GCT  
 362 W S G L S E G S V T C S S A S T T E D C 1 A L V L K G E A  
 1522 GAT GCC ATG AGT TTG GAT GGA TAT GTG TAC ACT GCA TGC AAA TGT GGT TTG GTG CCT GTC GCA GAG AAC TAC AAA TCC CAA  
 391 D A M S L D G Y V Y T A C K C G L V P Y L A E N Y K S Q  
 1609 CAA AGC AGT GAC CCT GAT CCT AAC TGT GTG GAT AGA CCT GTG GAA TAT CTT GCT GTG GCG GTG GTT AGG AGA TCA GAC ACT AGC  
 420 Q S D P D N C V D R P V E G Y L A V A V R R S D T S  
 1696 CTT ACC TGG AAC TCT GTG AAA GGC AAG AAG TCC TGC CAC ACC GCC GTG GAC AGG ACT GCA GGC TGG AAT ATC CCC ATG GGC CTG CTC  
 449 L T W N S V K G K K S C N T A V D R T A G W N I P M Q L L  
 1783 TTC AAC CAG ACC GGC TCC TGC AAA TTT GAT GAA TAT TTC AGT CAA AGC TGT GCC CCT GGG TCT GAC CCG AGA TCT AAT CTC TGT GCT  
 478 F N Q T G S C K F D E Y F S Q S C A P G S D P R S N L C A  
 1870 CTG TGT ATT GGC GAC GAG CAG GGT GAG AAT AAG TGC GTG CCC AAC AGC AAC GAG AGA TAC TAC GGC TAC ACT GGG GCT TTC CGG TGC  
 507 L C I G D E Q G E N K C V P N S N E R Y Y G Y T G A F R C  
 1957 CTG GCT GAG AAT GCT GGA GAC GTT GCA TTT GTG AAA GAT GTC ACT GTC TTG CAG AAC ACT GAT GGA AAT AAC AAT GAG GCA TGG GCT  
 536 L A E N A G D V A F V K D V T V L Q N T D G N N N E A W A  
 2044 AAG GAT TTG AAC CTG GCA GAC TTT GCG CTG CTG TGC CTC GAT GGC AAA CGG AAG CCT GTG ACT GAC GCT AGA AGC TGC CAT CTT GCC  
 565 K D L K L A D F A L L C L D G K R K P V T E A R S C H L A  
 2131 ATG GCC CCG AT CAT GCC GTG TCT CGG ATG GAT AAG GTG GAA CGC CTG AAA CAG GTG CTG CTC CAC CAA CAG GCT AAA TTT GGG  
 594 H A P N H A V Y S R M D K V E R L K Q V L L H Q Q A K F G  
 2218 AGA AAT GGA TCT GAC TGC CCG GAC AAG TTT TGC TTA TTC CAG TCT GAA ACC AAA AAC CTT CTG TTC AAT GAC AAC ACT GAG TGT CTG  
 623 R N G S D C P D K F C L F Q S E T K N L L F N D N T E C L  
 2305 GGC AGA CTC CAT GGC AAA ACA ACA TAT GAA AAA TAT TTG GGA CCA CAG TAT GTC GCA GGC ATT ACT AAT CTG AAA AAG TGC TCA ACC  
 652 A R L H G K T T Y E K Y L G P Q Y V 1 A G 1 T N L K K C S T  
 2392 TCC CCC CTC CTG GAA GCC TGT GAA TTC CTC AGG AAG TAA AACCGAAGAA GATGGCCAG CTCCTAACAGC CATTCACTGC CCCAACGCTCT  
 681 S P L L E A C E F L R K D  
 2491 TCTCCCCAGG TGTGTTGGG CCTTGGCTCC CCTGCTGAAG GTGGGGATTG CCCATCCATC TGCTTACAAT TGCTCTGTGT CGTCTTAGCA AGAAGTAAAAA  
 2591 TGAGAAATT TGTTGATATT CAAAAAA

FIG-2B

RESTRICTION MAP OF 5' - FLANKING REGION OF  $\alpha$ S1 CASEIN GENE



S - Sall

B - BamHI

R - EcoRI

H - HindIII

M - SmaI

N - NcoI

NS - NsiI

X - XbaI

K - KpnI

FIG.-3

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

RESTRICTION MAP OF 3' FLANKING  
REGION OF  $\alpha$ S1 CASEIN GENE

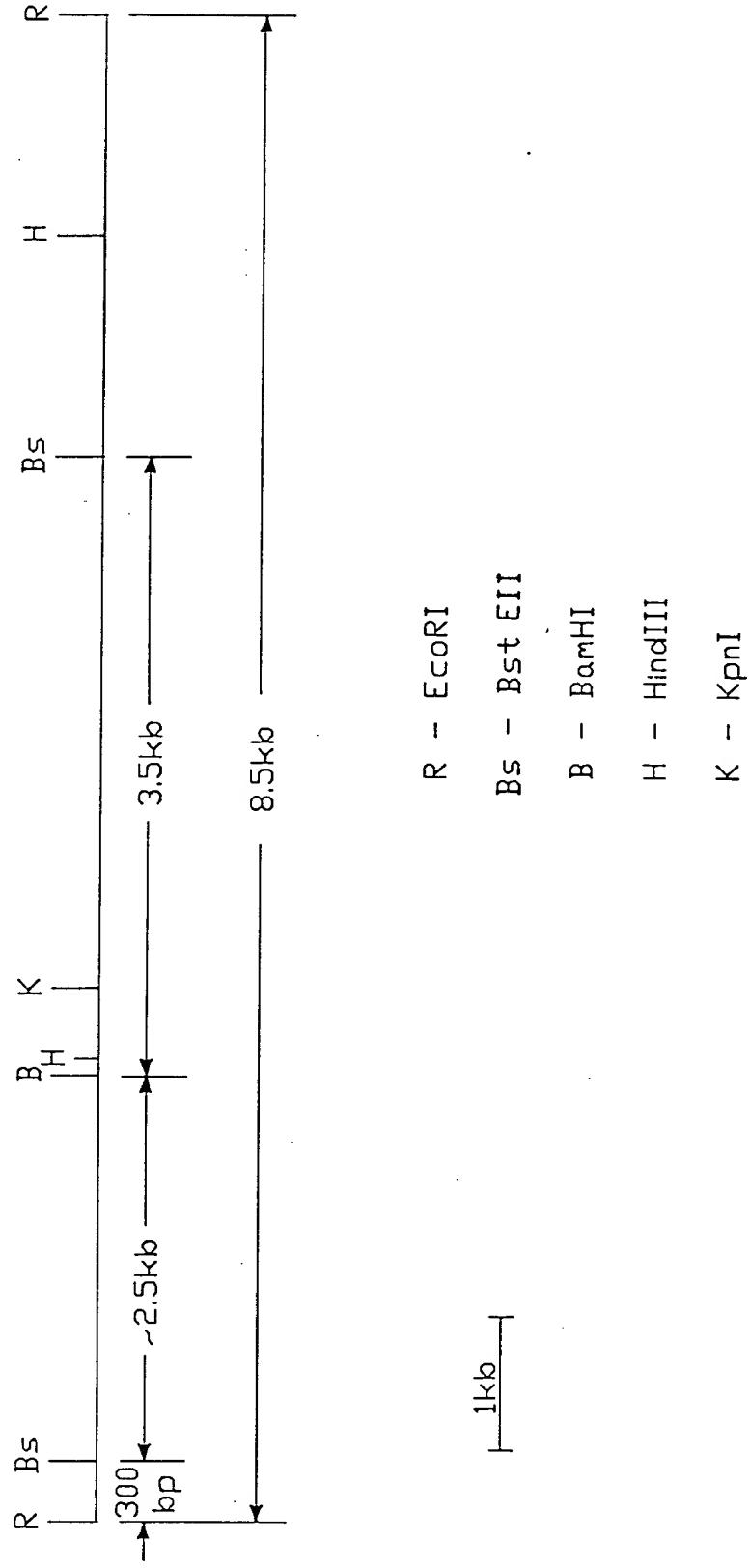
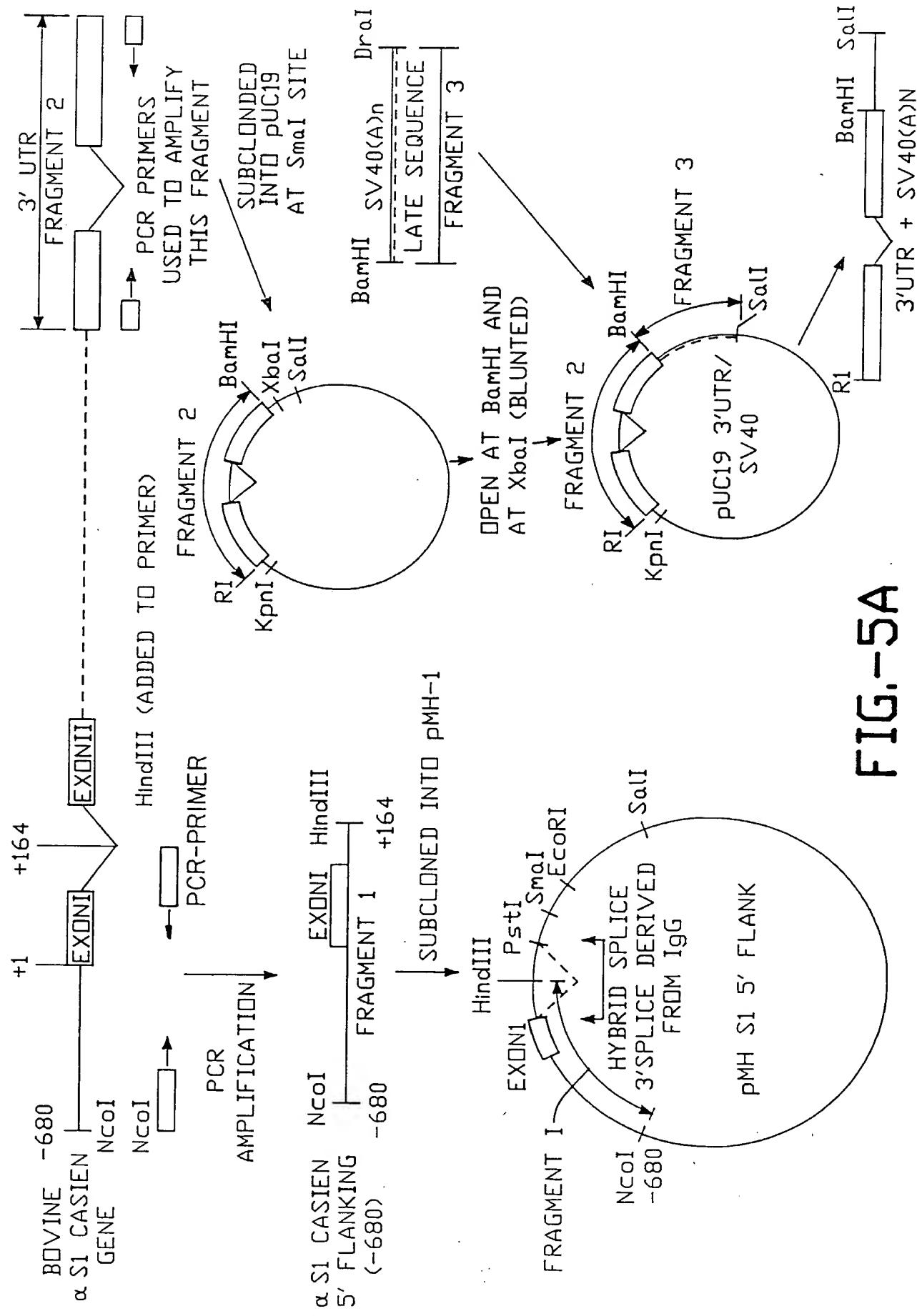
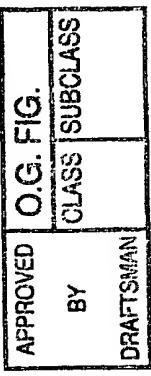


FIG.-4



**FIG.-5A**

APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
	DRAFTSMAN

ISOLATE NcoI - EcoRI FRAGMENT  
pMHS1 5' FLANK

ISOLATE EcoRI - SalI FRAGMENT FROM  
pUC19 3'UTR/5V40

## SUBCLONE IN PMH-1 CUT WITH NC81 - S81

NCOI-680

PS1 3' 5' FLANK

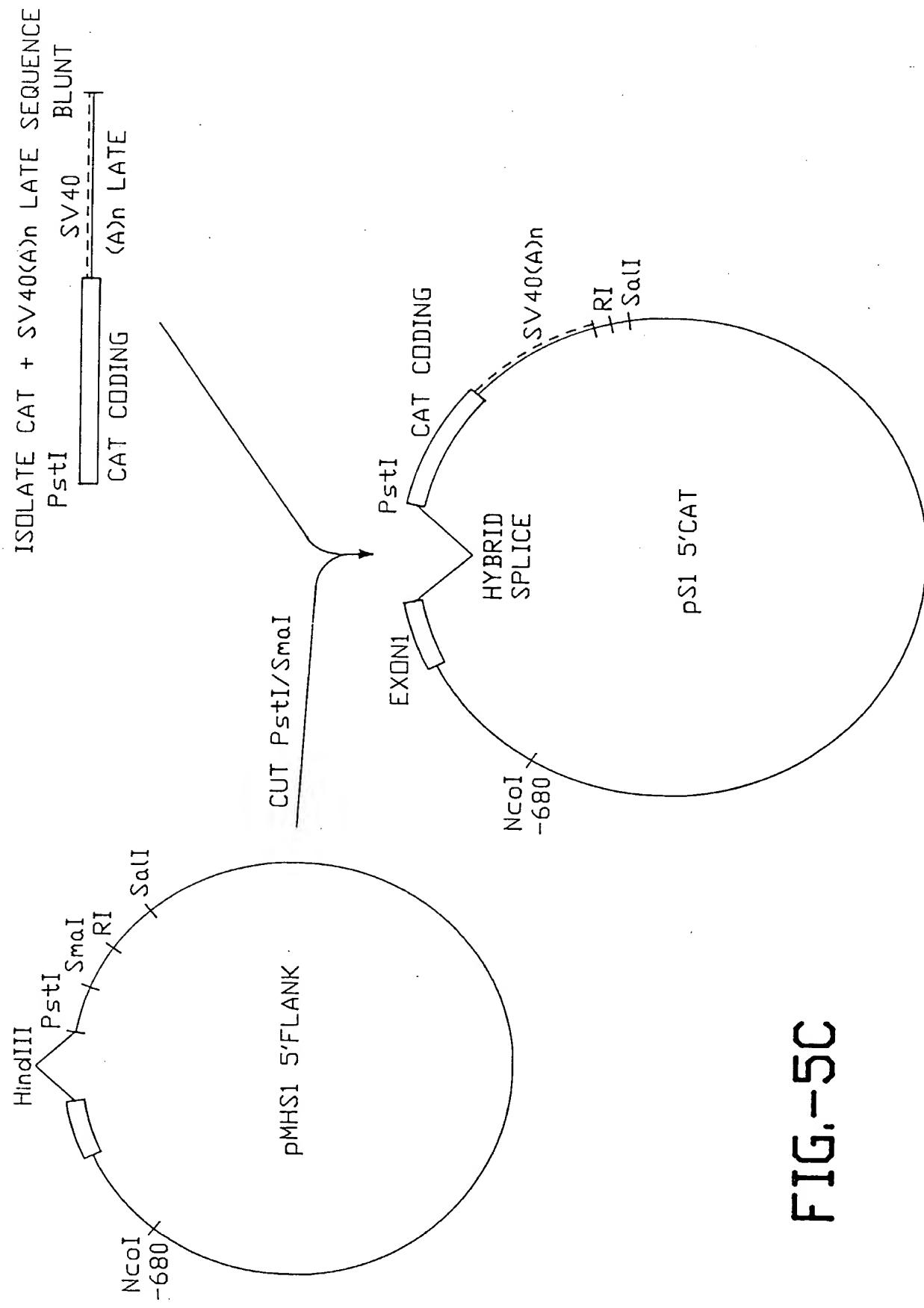
CAT FRAGMENT 4 /  
PstI BamHI (MADE BLUNT-ENDED  
WITH KLENOW)

CUT WITH PstI  
AND SmaI;  
LIGATE WITH  
FRAGMENT A

DS13'5'CAT

FIG.-5B

APPROVED	O.G. FIG.
By	CLASS
DRAFTSMAN	SUBCLASS



APPROVED	O.G. FIG.
CLASS	SUBCLASS
BY	DRAFTSMAN

NAME pMH-1

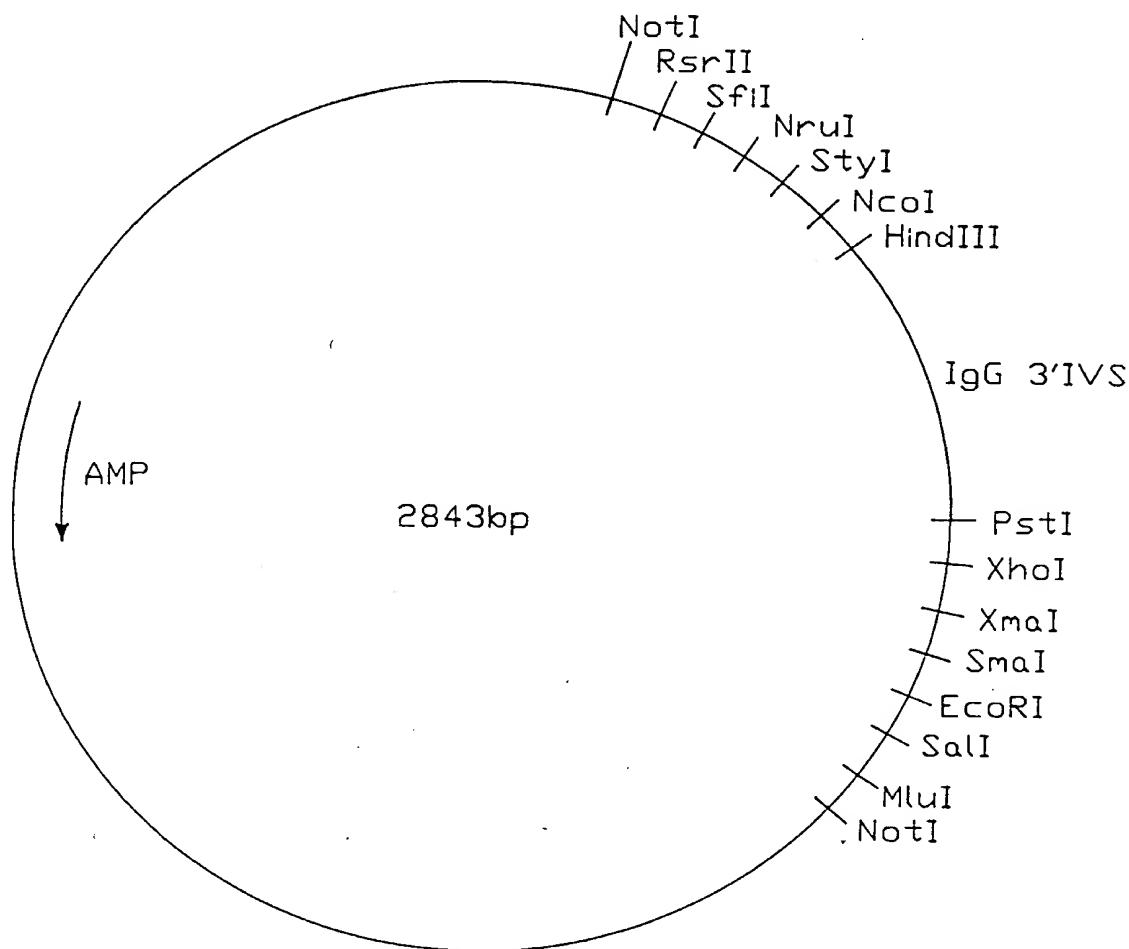
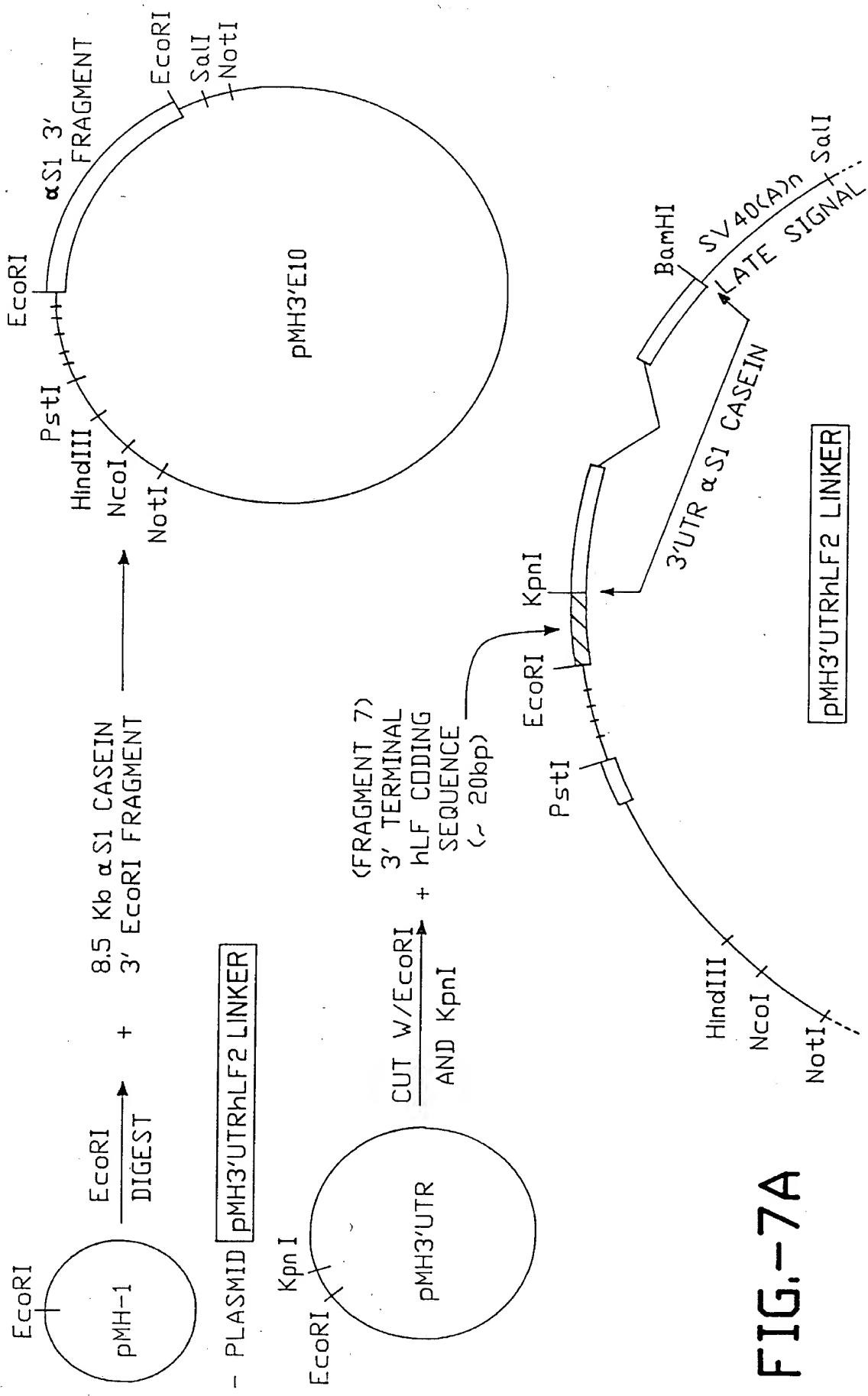


FIG.-6

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

- PLASMID **PMH3'E10** CONTAINS ~ 8.5Kb EcoRI FRAGMENT OF THE 3'-END OF  $\alpha$  S1 CASEIN. PMH-1 WAS CUT w/EcoRI + LIGATED TO THIS FRAGMENT



**FIG.-7A**

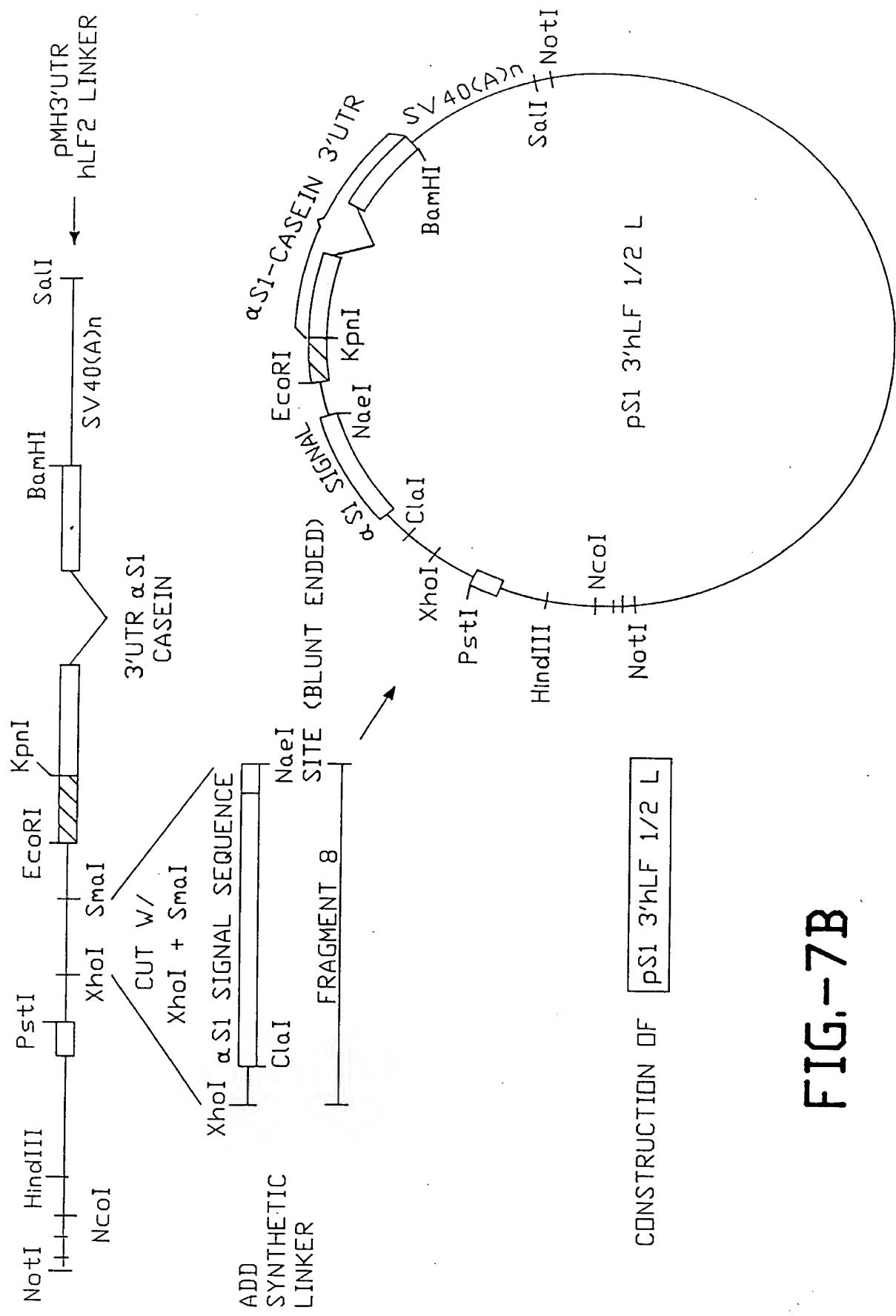
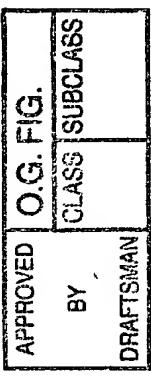
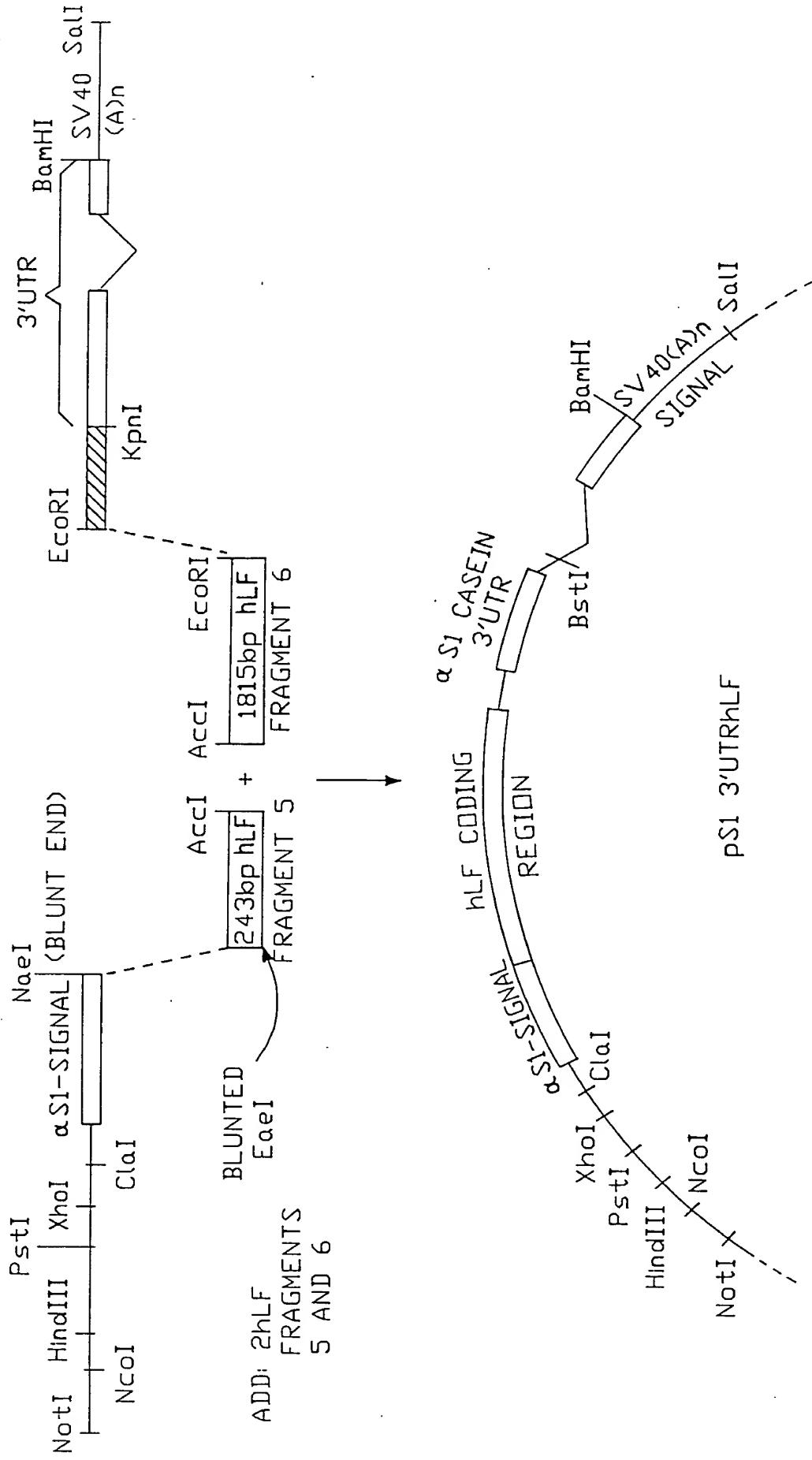


FIG.-7B

APPROVED	O.G. FIG.
BY	CLASS
	SUBCLASS
	DRAFTSMAN

## CONSTRUCTION OF pS1 3'UTR hLF

PSI 3' hLF 1/2 L CUT w/ Nael AND ECORI

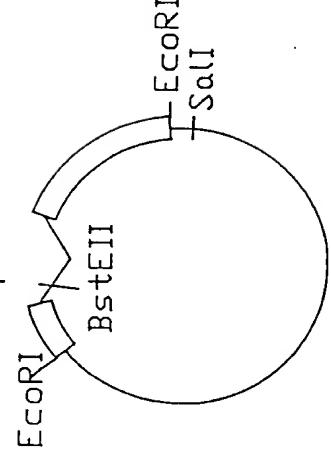


pS1 3'UTR hLF

FIG.-7C

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

STARTED w/pMH3'E10



CONSTRUCTION OF

pLF3' 10kb

ISOLATED THE BstEII TO SalI FRAGMENT



PURIFIED THE LARGE BstEII/SalI  
FRAGMENT FROM P51 3'UTR hLF AND  
LIGATED THE BstEII/SalI FRAGMENT,

LIGATED

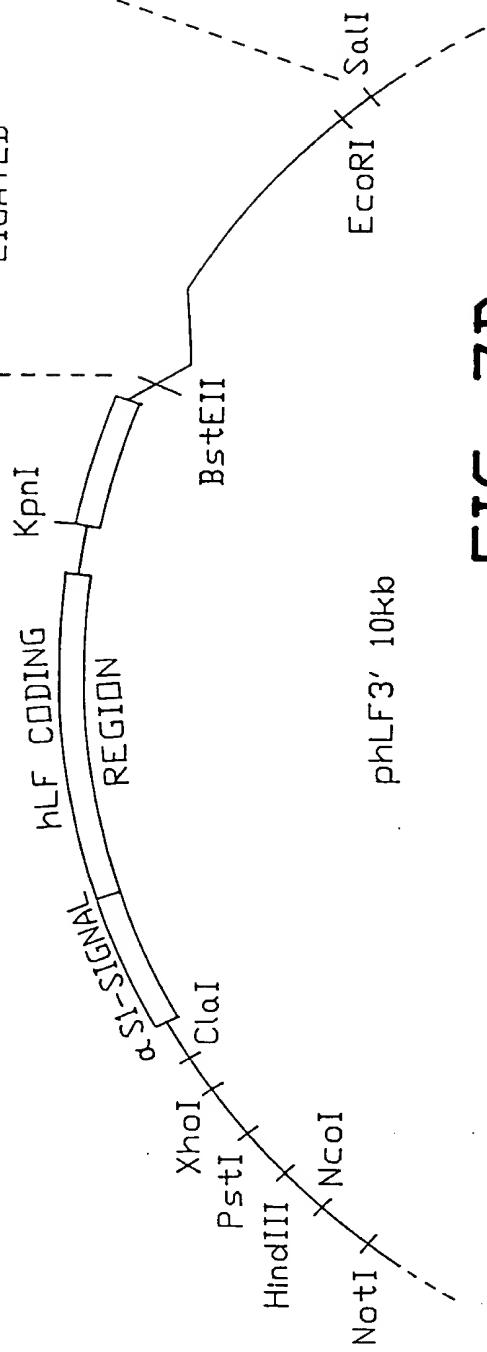
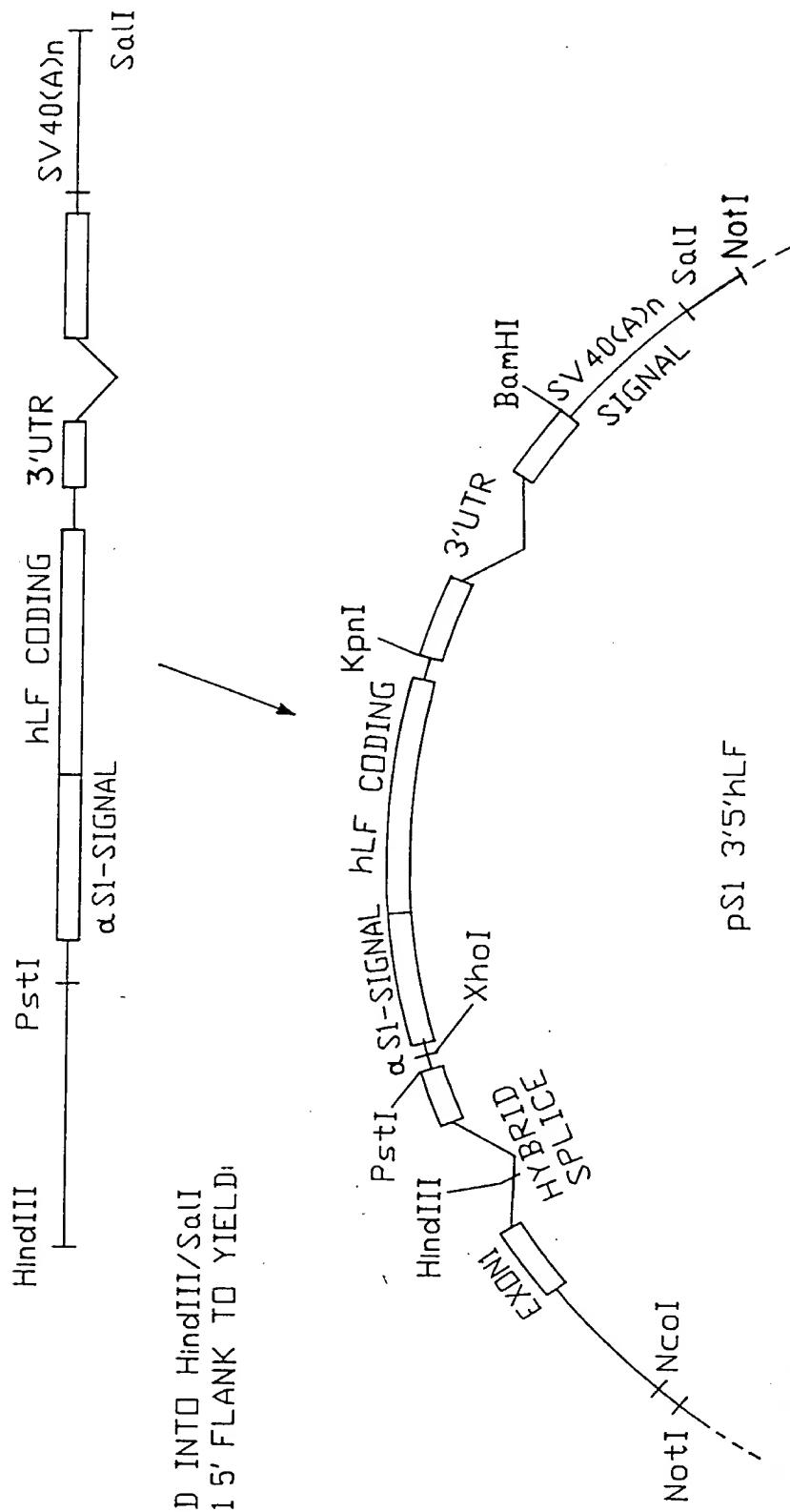


FIG.-7D

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

CONSTRUCTION OF PS1 3'5'hLF

STARTED w/PS1 3'UTR hLF, CUT w/HindIII AND SalI AND PURIFIED THIS FRAGMENT CONTAINING THE  $\alpha$ S1-CASEIN SIGNAL SEQUENCE, hLF CODING REGION,  $\alpha$ S1UTR AND SV40(A)n.

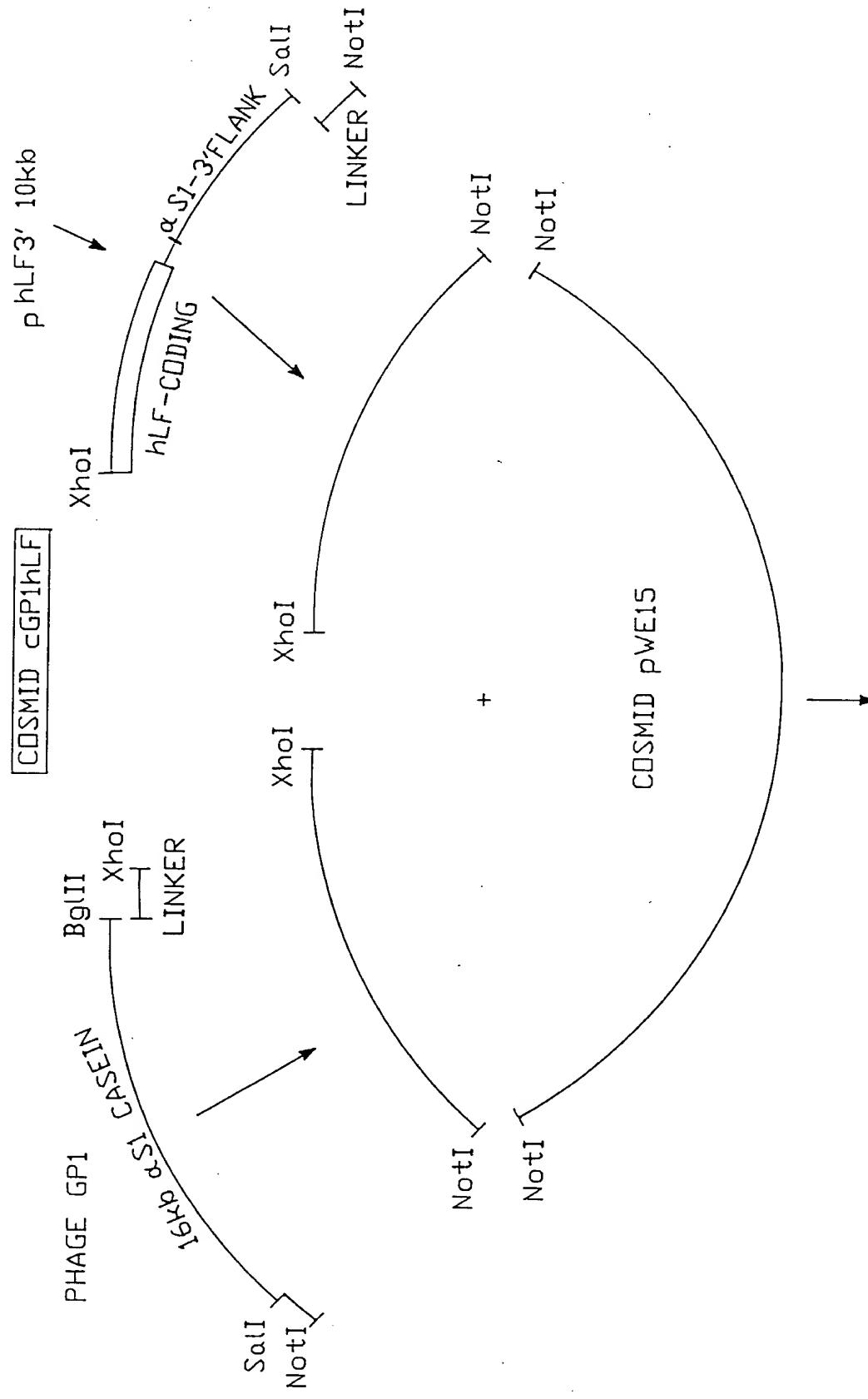


SUBCLONED INTO HindIII/SalI  
CUT PMHS1 5' FLANK TO YIELD:

NOTE: PS1 5'hLF WAS MADE BY CUTTING PS1 3'5'hLF w/KpnI AND BamHI, FOLLOWED BY BLUNTING THE ENDS AND RELIGATING. THIS ELIMINATES THE SPLICED 3'UTR REGION.

**FIG.-7E**

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS



3 WAY LIGATION, THE DNA FROM THIS COSMID IS PREPARED BY CUTTING WITH **NotI** AND PURIFYING THE EXPRESSION SEQUENCE PRIOR TO MICROINJECTION.

**FIG.-7F**

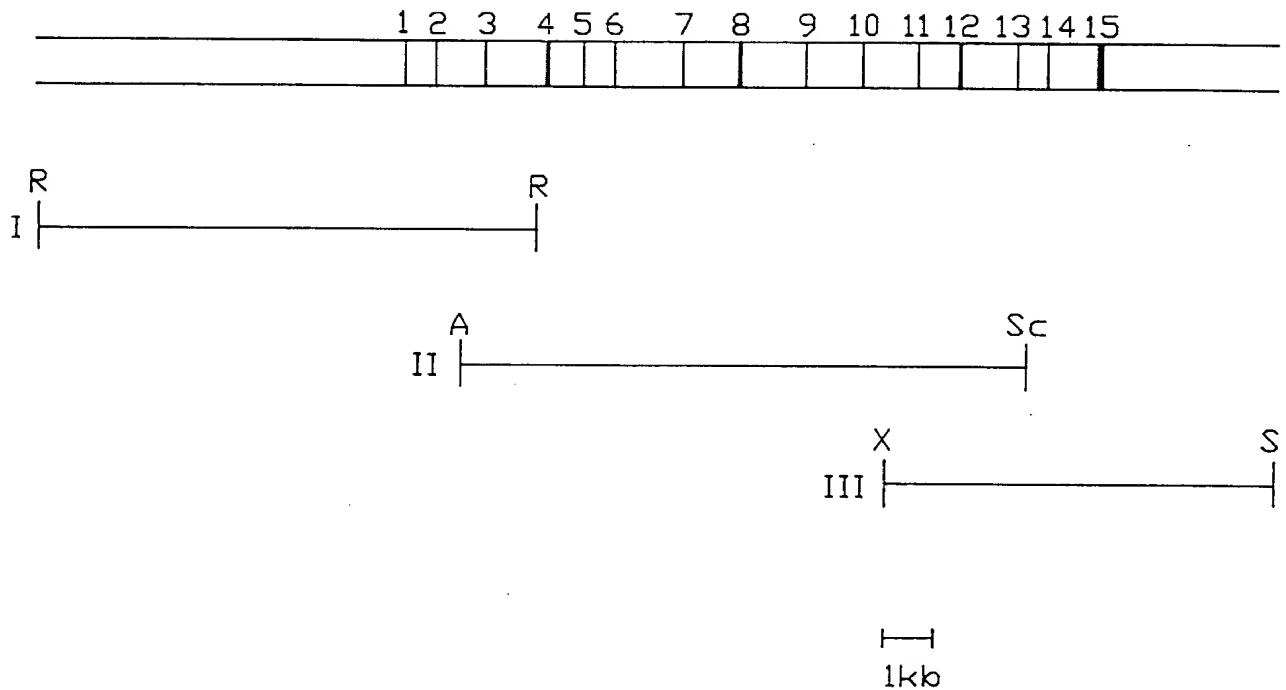


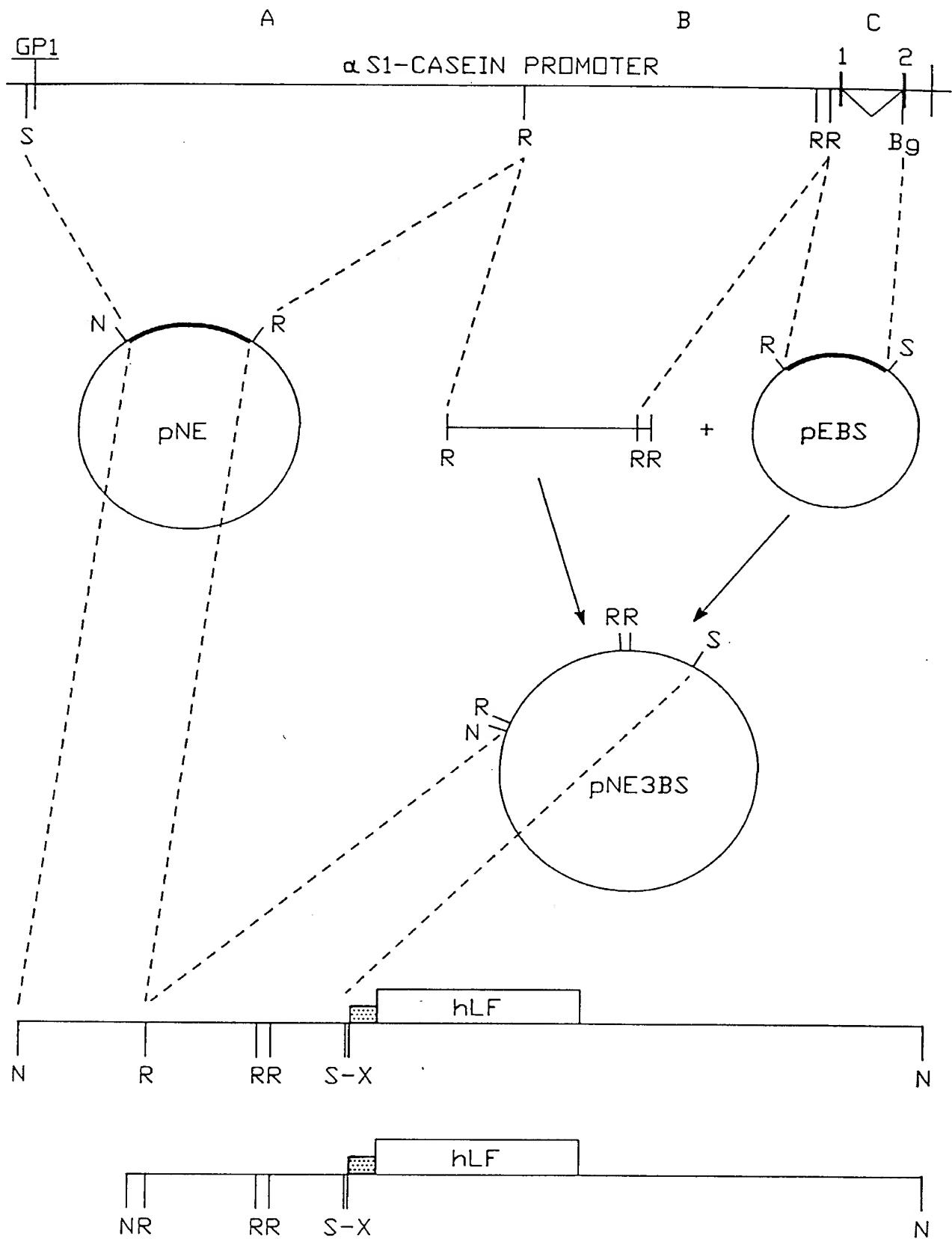
FIG.-8A

BstEII 18000

NcoI 8079 9374

NcoI x HindIII 4245 3593 2814 6209

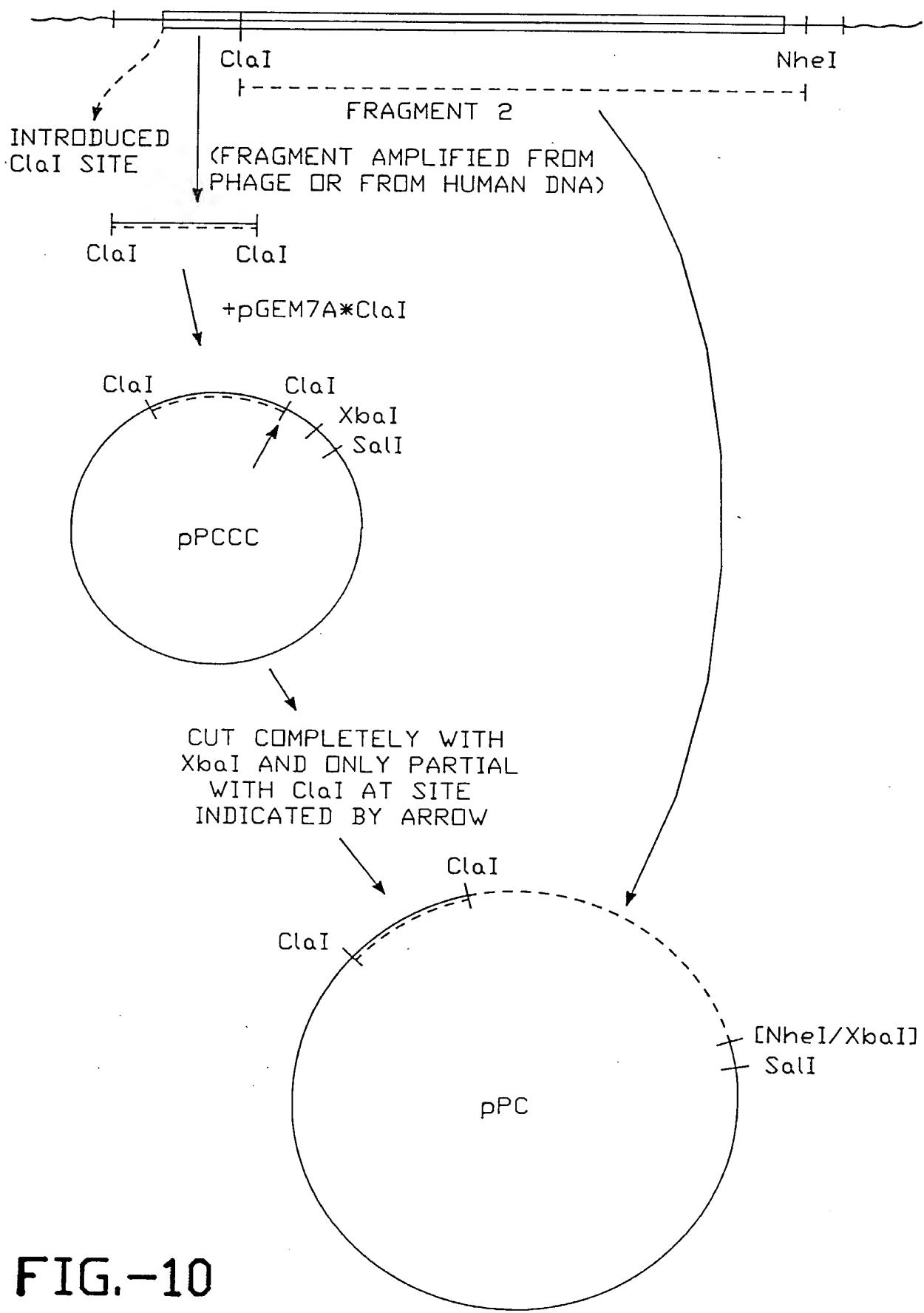
FIG.-8B



S=SalI R=EcoRI Bg=BglII N=NotI X=XbaI

FIG.-9

PHAGE CONTAINING PROTEIN C GENE



O.G. FIG.	
CLASS	SUBCLASS
BY	
DRAFTSMAN	

5'- ATCACCTTGA TCATCAACCC AGCTTGCTGC TTCTTCCCAG  
TCTTGGGTTC AAG gtattatgt tacatataac aaaatttcta tgat~~ttt~~cct ctgtctcatc  
tttcat~~t~~ttt cataatacg cagttgtaac ttttctatgt gattgcagt attggtactt tcctatgata  
tactgttagc aagcttgagg tgtggcaggc ttgagatctg gccatacact tgagtgacaa tgacatccac  
tttgcctttc tctccacag GTGTCCACTC CCAGGTCCAA CTGCAG -3'

FIG.-11

APPROVED	O.G. FIG.
CLASS	SUBCLASS
BY DRAFTSMAN	

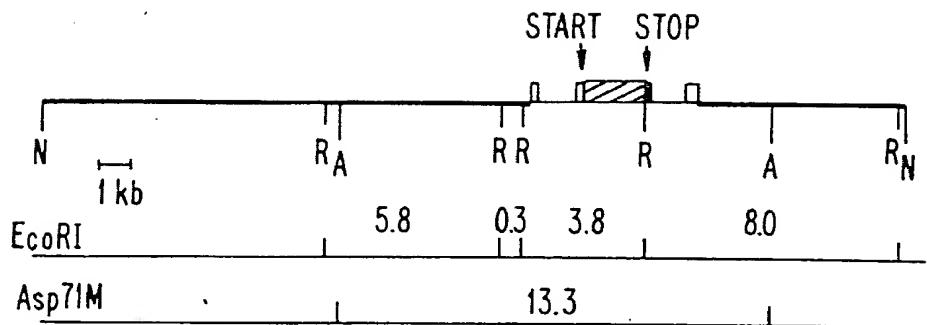


FIG. 12A.

COSMIDS CONTAINING ENTIRE hLF GENE (NOT DRAWN TO SCALE)

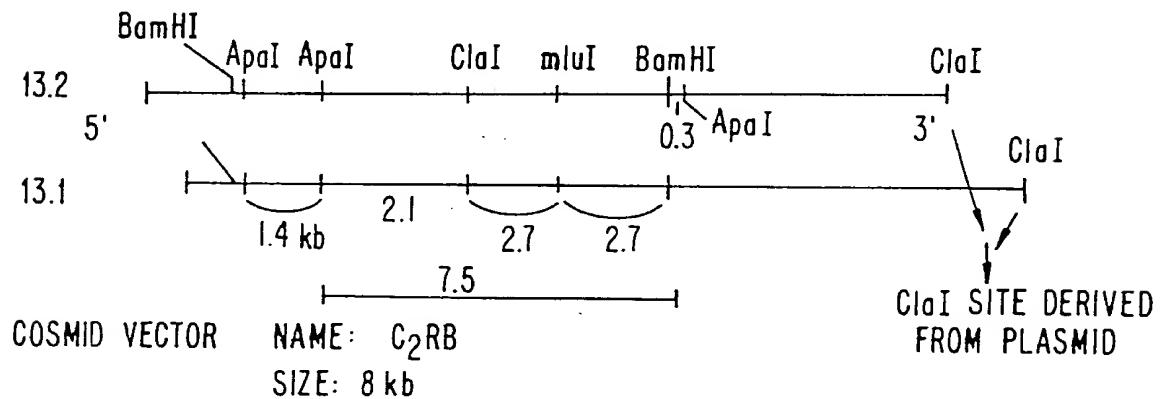


FIG. 13.

9 kb Bam HI hLF FRAGMENT IN pUC19

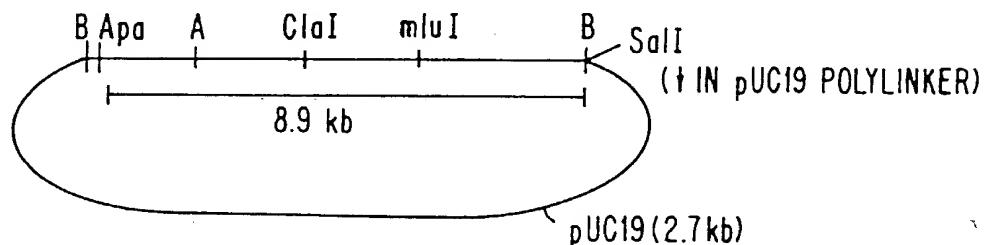


FIG. 14.

APPROVED	O.G. FIG.
	CLASS
BY	SUBCLASS
DRAFTSMAN	

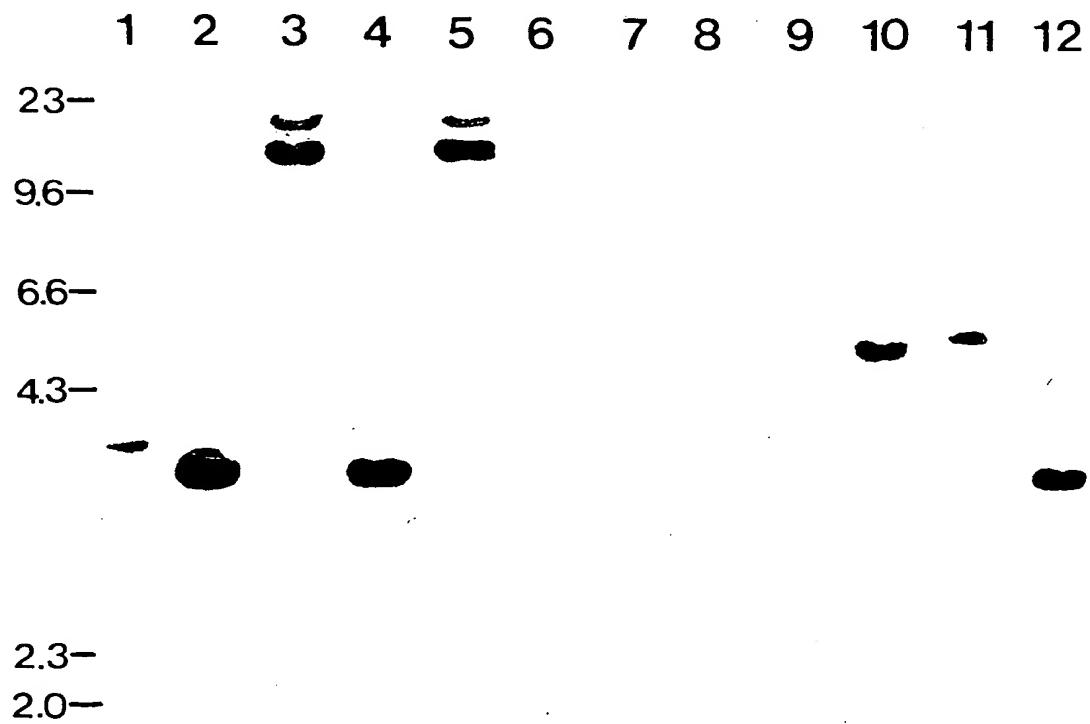
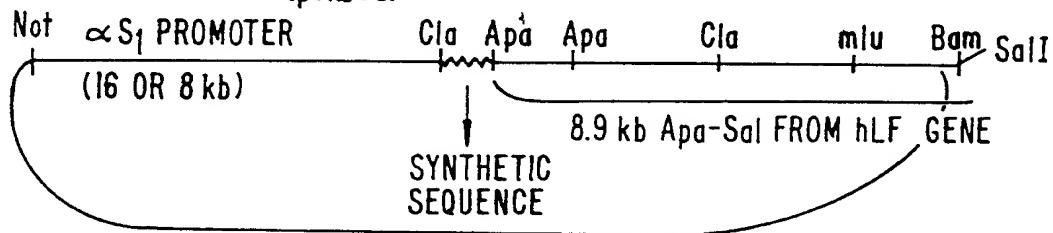


FIG. 12B.

LIGATION PRODUCT OF p16kbCS AND SYNTHETIC SEQ. (Cla-Apa)+ hLF FRAGMENT  
(p8kbCS)

APPROVED	O.G. FIG.
CLASS	SUBCLASS
BY	
DRAFTSMAN	



CLONING VECTOR: pkUN (4 kb)  
CONSTRUCT NAME: 8 hLF gen 9k, OR 16 hLF gen 9k

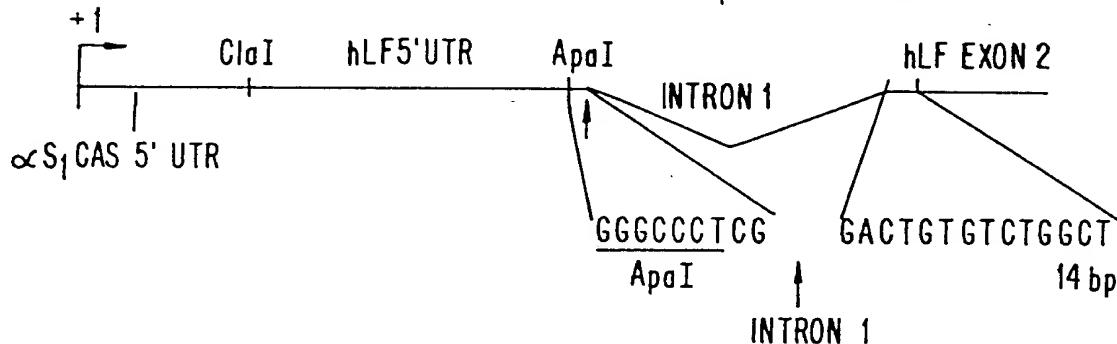
FIG. 15A.

STRUCTURE OF ClaI-ApaI SYNTHETIC SEQUENCE

$\text{ClaI}$ 5'-CGA TAC CAA GTC GCC TCC AGA CCG CAG ACA TGA AAC TTG TCT T ATG GTT CAG CGG AGG TCT GGC GTC TGT ACT TTG AAC AGA	TRANSLATION INITIATION CODON   T
<hr/> TCC TCG TCC TGC TGT TCC TCG GGG CC 3' AGG AGC AGG ACG ACA AGG AGC C	
$\text{NpaI}$	

FIG. 15B.

+1: TRANSCRIPTION INITIATION SITE OF BOVINE  $\alpha$ S<sub>1</sub>-CASEIN GENE



STRUCTURE OF REGION CONTAINING EXON 1 (HYBRID  $\alpha$ S<sub>1</sub>-CASEIN/hLF EXON) AND PART OF EXON 2 OF THE GENOMIC hLF CONSTRUCTS DEPICTED IN FIGS. 15A THROUGH 17.

FIG. 15C.

COINJECTION

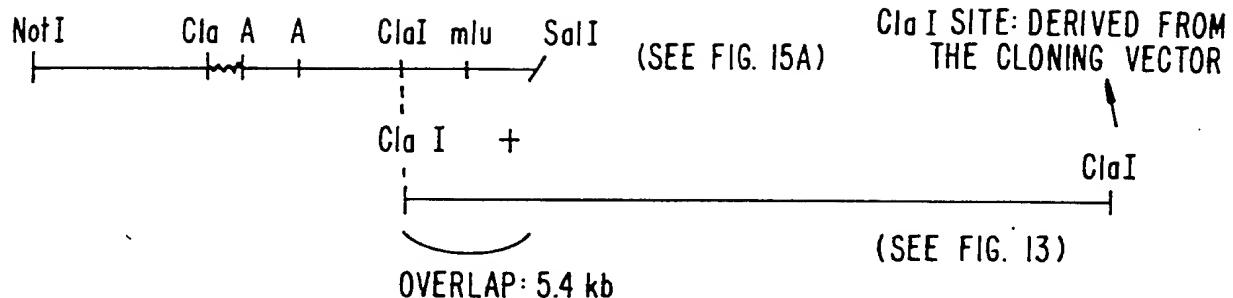
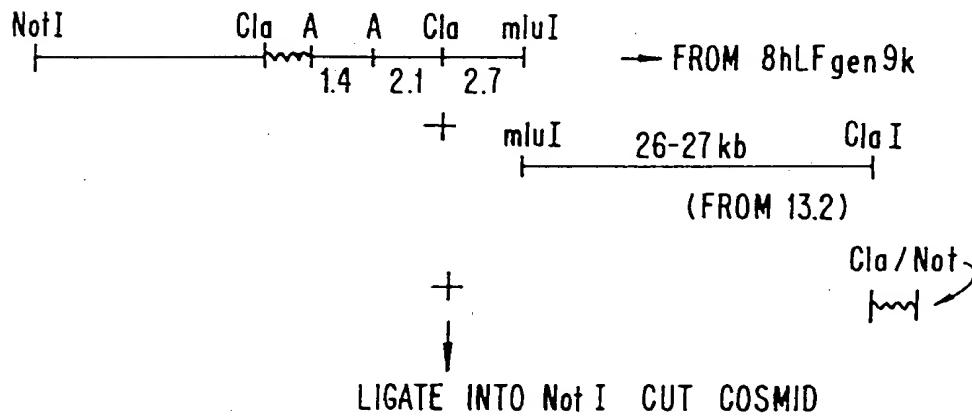


FIG. 16.

APPROVED	O.G. FIG.
CLASS	SUBCLASS
BY DRAFTSMAN	

GENERATION OF 8hLF GENE



Cla/Not LINKER:      SalI

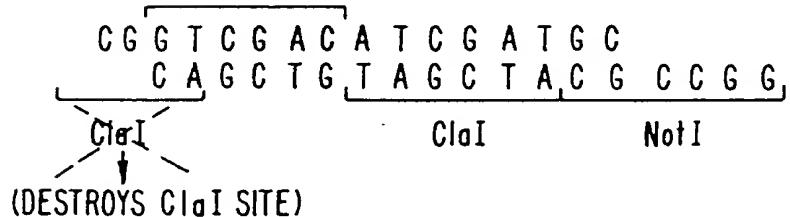


FIG. 17.

APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
	DRAFTSMAN

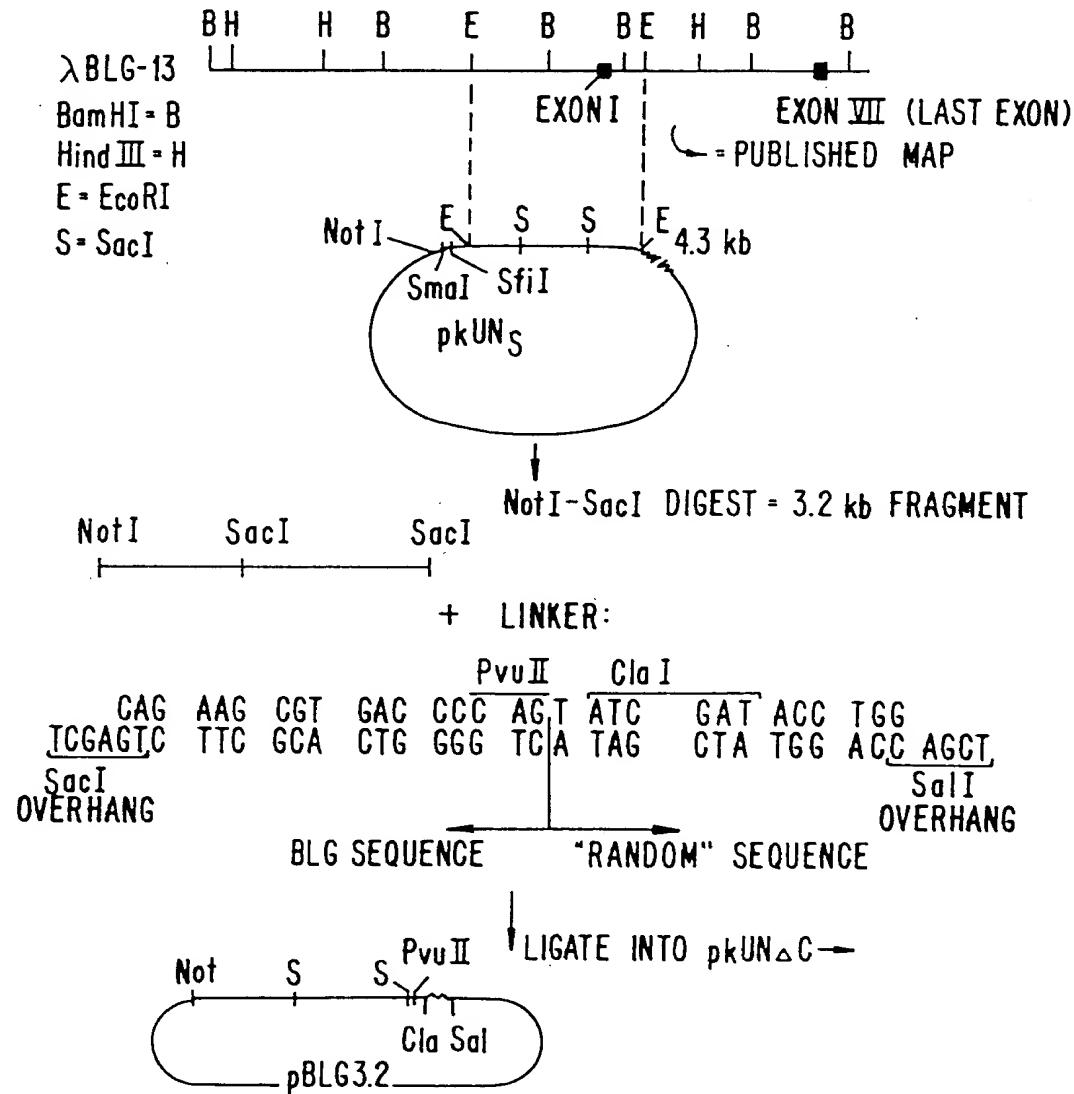


FIG. 18.

APPROVED	O.G. FIG.
CLASS	SUBCLASS
BY DRAFTSMAN	

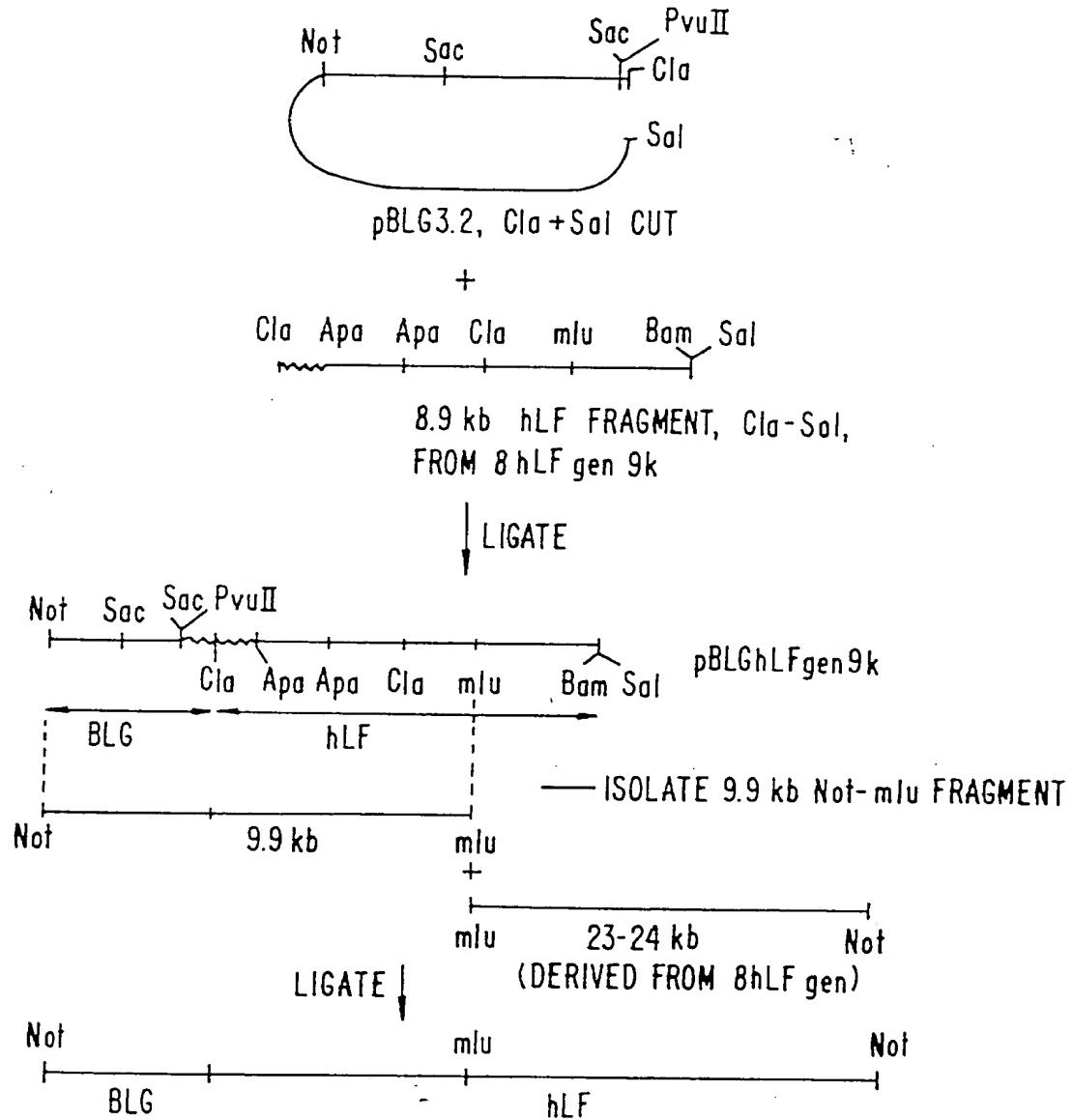


FIG. 19.

APPROVED	O.G. FIG.
CLASS	SUBCLASS
BY	DRAFTSMAN

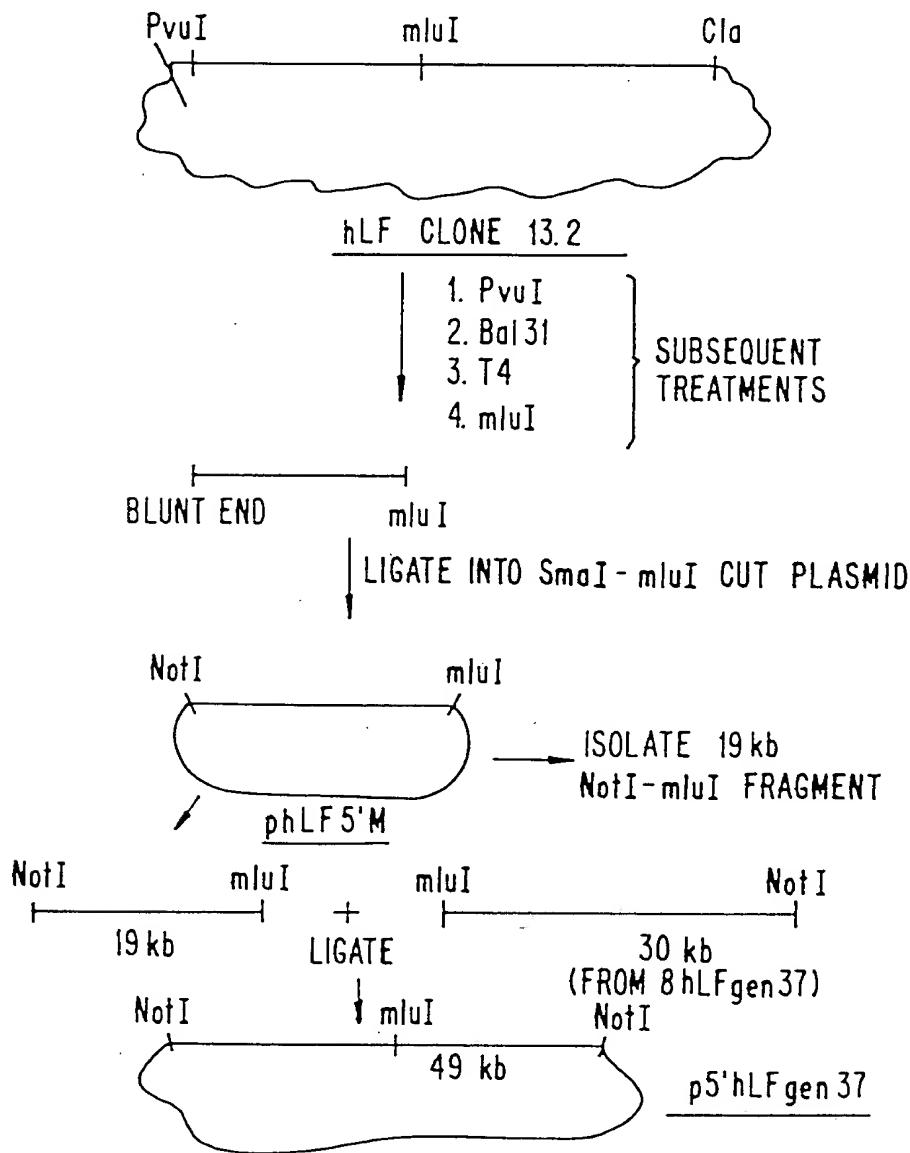


FIG. 20.

APPROVED	O.G. FIG.
CLASS	SUBCLASS
BY DRAFTSMAN	

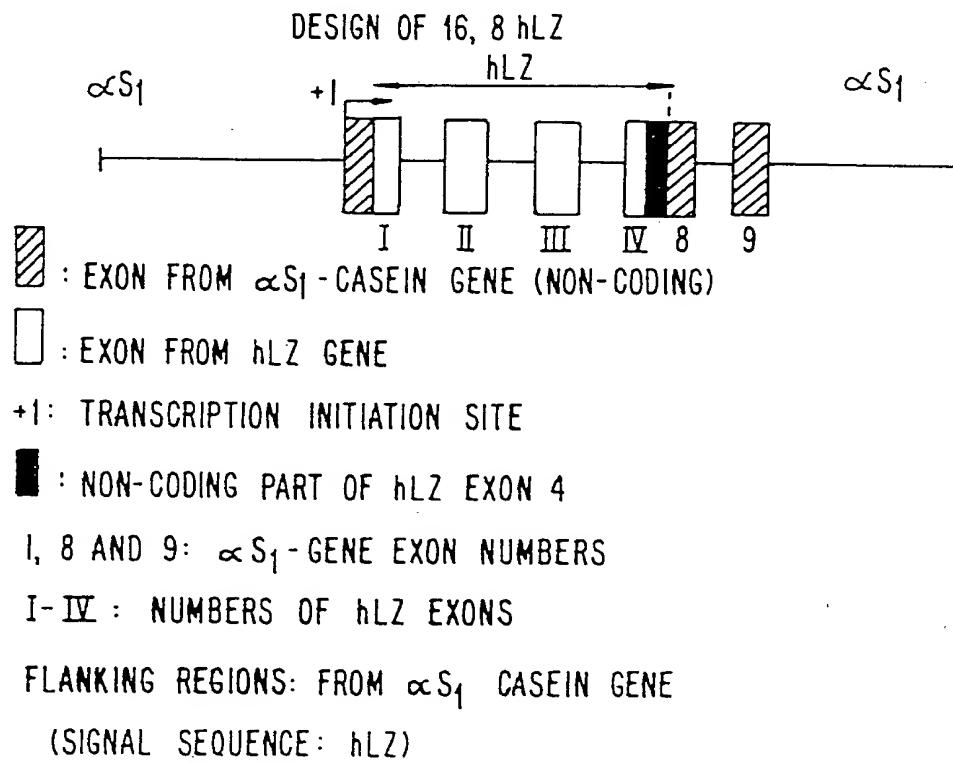


FIG. 21.

DESIGN OF 16, 8 hLZ3

LEGEND: SEE FIGURE 9

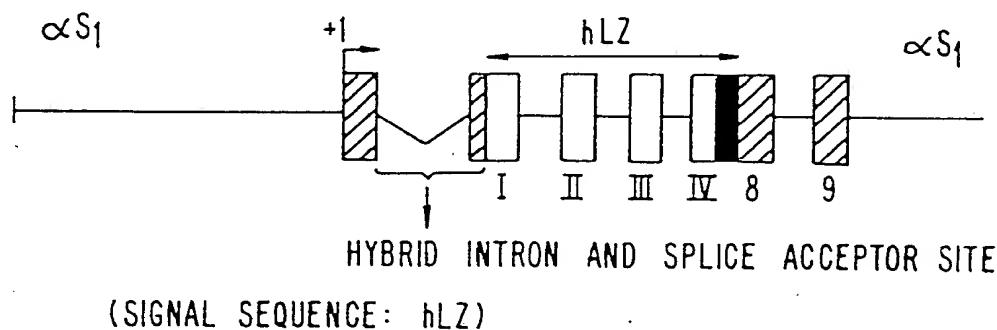
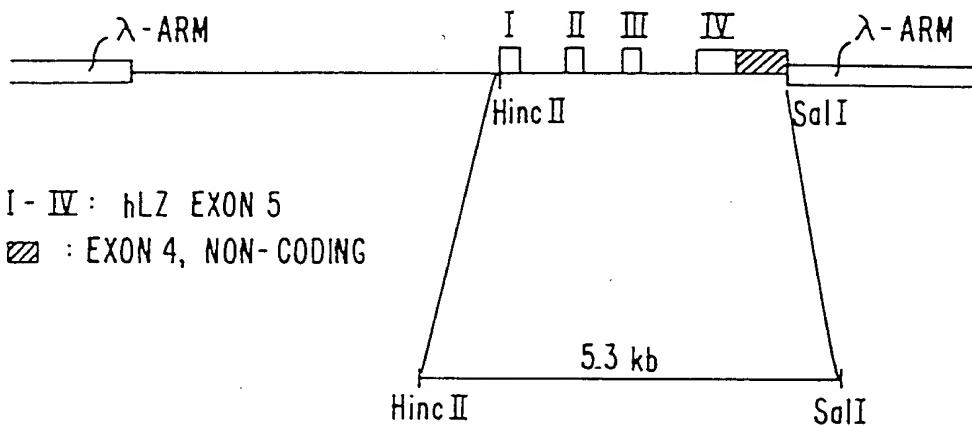


FIG. 22.

λ7.2.1



I - IV: hLZ EXON 5  
▨ : EXON 4, NON-CODING

APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

PRIMERS:

+3: 5'UTR hLZ

CAT G G T A G C T A G G G A T C G T G A G A C T G G A T C G T C A G  
CAT A T C G A T C C C T A G C A C T C T G A C C T A G C A G T C  
Kpn I                    Cl a I    Hinc II

LIGATE 5.3 Hinc II - Sal I  
Kpn - Hinc II

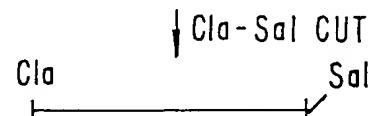
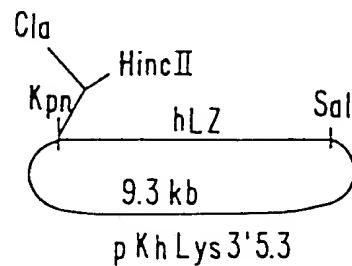


FIG. 23A.

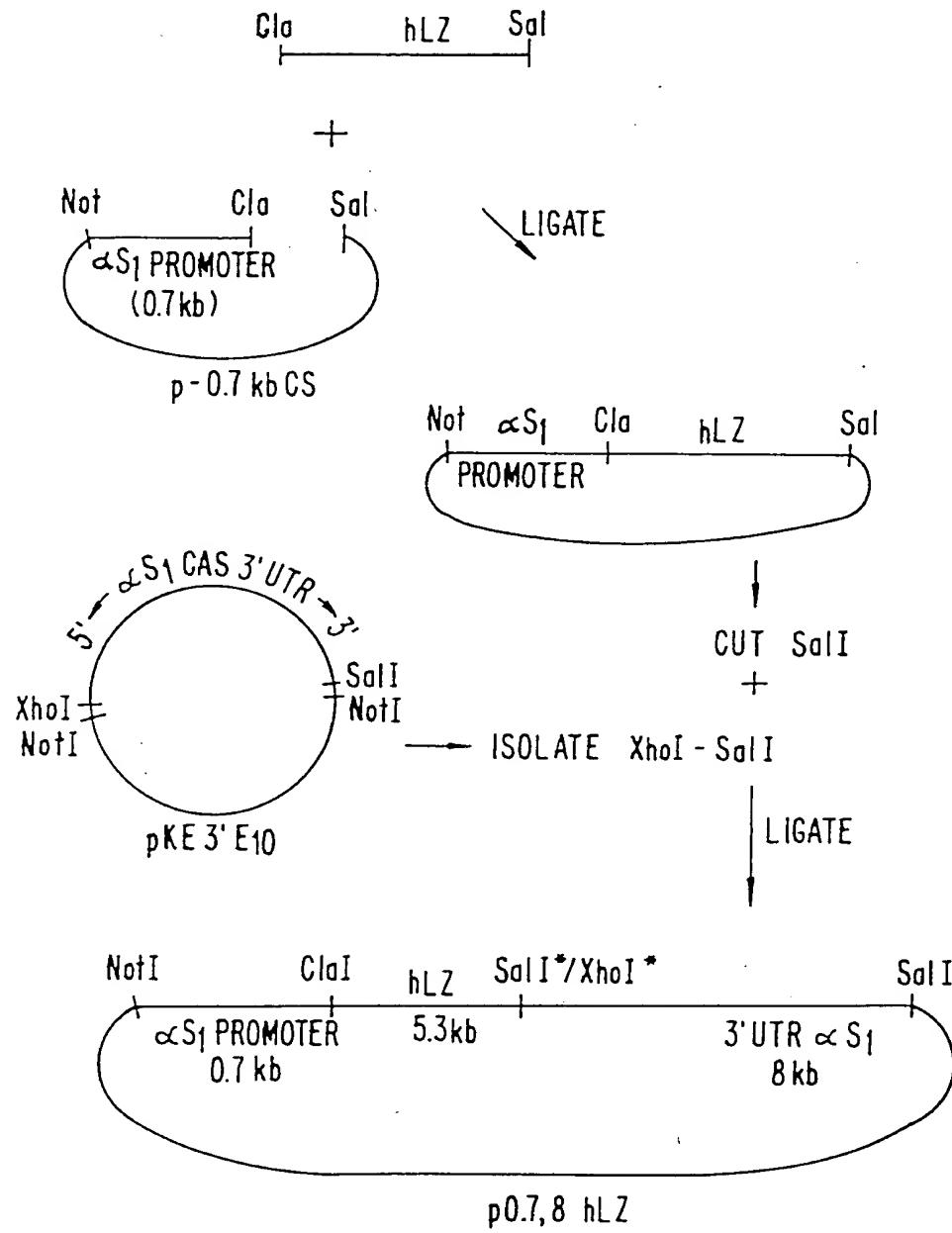
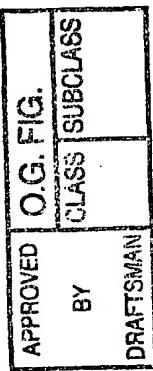


FIG. 23B.

LINKER S<sub>1</sub>/S<sub>2</sub>:

SalI<sup>\*</sup>-NotI-SalI<sup>\*</sup>

⊗ - DESTROYED SITE

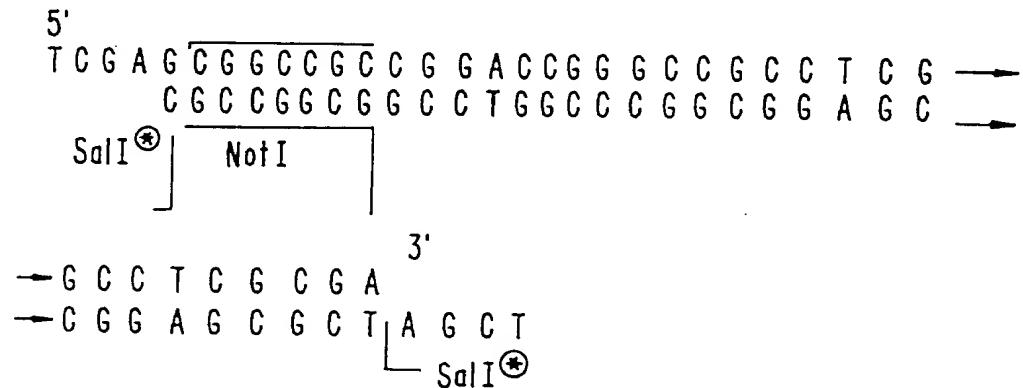


FIG. 23C.

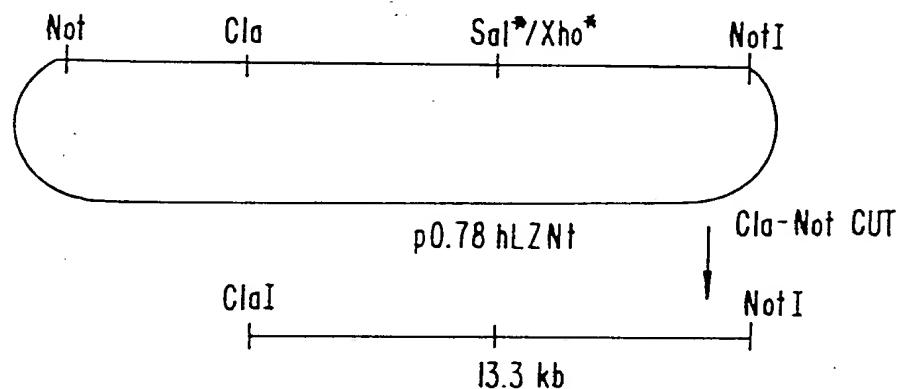
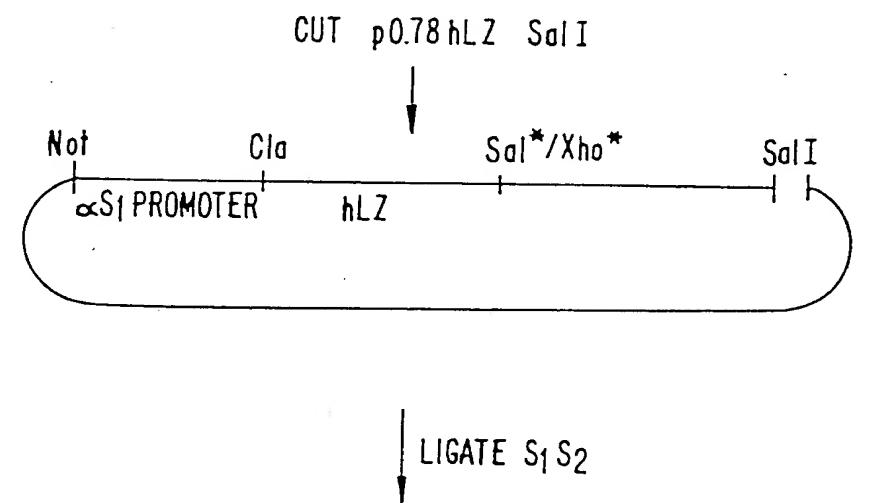


FIG. 23D.

APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

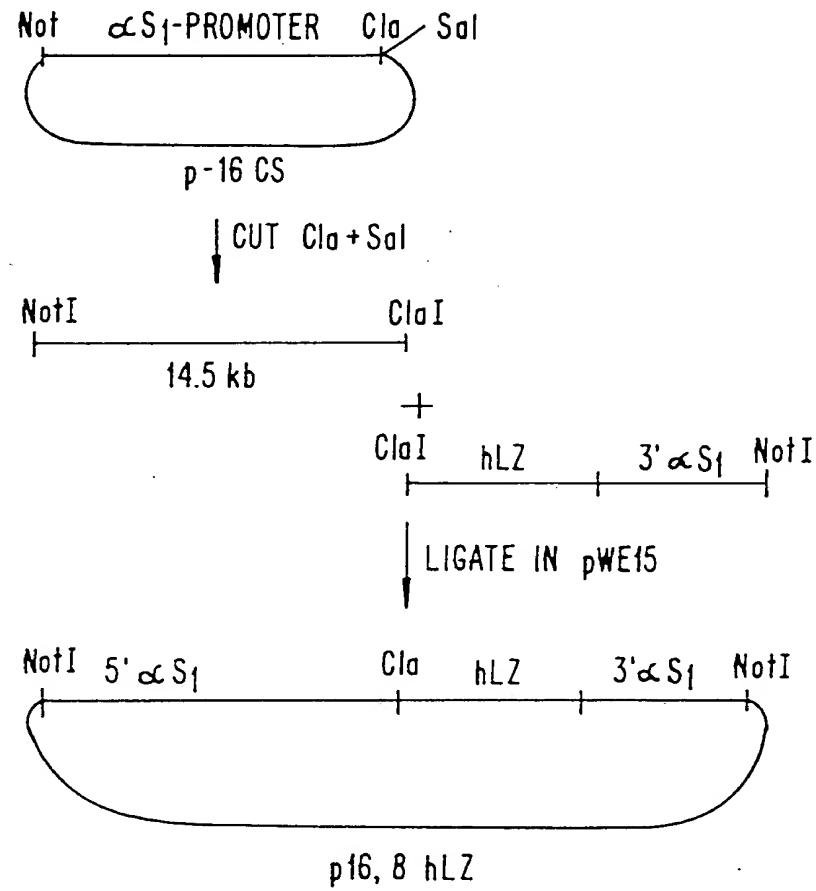


FIG. 23E.

APPROVED	O.G. FIG.
BY	CLASS
	SUBCLASS
	DRAFTSMAN

BOVINE 2	GGAAGTGCCTGGAGA...TTAAAATGTGAGAGTGGAGT...GGAGGTTG	44
SHEEP 84	GGAAGTGTCTGGAGATTTAAAATGTGAGAGGCGGGAGGTGGAGGTTG	133
45	GGTCTGTAGGCCTTCCATCCCACGTGCTCACGGAGCCCTAGTGCTAC	94
134	GGCCTGTGGCCTGCCATCCCACGTGCCTGCATTAGCCCCAGTGCTGC	183
95	TCAGTCATGCCCGCAGCAGGGTCAGGTCACTTCCCACCTGGGGT	144
184	TCAGCCGTGCCCGCAGGGTCAGGTCACTTCCCCT. GGGGT	232
145	TATTATGACTGTTGTCATTGTTGCCATTGGCTACCTGGGCTACCTGGG	194
233	TATTATGACTCTGTCATTGCCATTGCCATTGGCTACCTGGGCTACCTGGG	282
195	AGCGGGTGCTTGCAGAGCCCTCGATACTGACCAGGTTCCCCCTCGGAGC	244
283	AGCAGGTGCTTGCAGAGCCCTCGATAACCGACCAAGG. TCCTCCCTCGGAGC	331
245	TCGACCTGAACCCATGTCACCCCTGCCAGCCTGCAGAGGGTGGTGA	294
332	TCGACCTGAACCCATGTCACCCCTGCCAGCCTGCAGAGGGTGGTGA	381
295	CTGCAGAGATCCCTTACCCAGGCCACAGTCACATGGTTGGAGGAGAT	344
382	CTGCAGAGATCCCTTACCCAGGCCACGGTCACATGGTTGGAGGAGCT	431
345	GGTCCCCAAGGCAGAAGCCACCCCTCCA. GACACACCTGCCAGTGCTG	393
432	GGTCCCCAAGGCAGAGGCCACCCCTCCAGGACACACCTGTCAGTGCTG	481
394	GCTCTGACCTGTCCTGTCATAAGAGGCTGACCCAGAAGTGTTCCTGGCG	443
482	GCTCTGACCTGTCCTGTCATAAGAGGCTGACCCGGAAAGTGTTCCTGGCA	531
444	CTGGCAGCCAGCCTGGACCCAGGCCCTGACACCC. CCTGCCCCCCACT	492
532	CTGGCAGCCAGCCTGGACCCAGAGTCAGACACCCACCTGTCAGGCGCT	581
493	TCTGGGGCGTACCAAGGAACCGTCCAGGCCAGA..GGGCCTTCCTGCTT	540
582	TCTGGGGTC.TACCAAGGAACCGTCTAGGCCAGAGGGGACTTCCTGCTT	630
541	GGCCTCGAATGGAAGAAGGCCCTCTATTGTCCTTCGTAAGGAAGCAACC	590
631	GGCCTTGGATGGAAGAAGGCCCTCTATTGTC. TCGTAGAGGAAGCCACC	679
591	CCAGGGCCCAAGGATAGGCCAGGGGGATTGGGGAAACCGCGTGGCT. CC	639
680	CCGGGGCCTGAGGATGAGCCAAGTGGGATTCCGGGAACCGCGTGGCTGGG	729
640	GGCGGGGCCGGCTGGCTGGCTGGC..CCTCCTCCTGTATAAGGCCCG	687
730	GGCCCAGCCGGCTGGCTGGCTGGCATGCGCCTCCTGTATAAGGCCCA	779

FIG. 24A.

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
		DRAFTSMAN

\*TRANSLATION INITIATION CODON

FIG. 24B.

LINKER GP 278/279

ClaI      TRANSLATION START SITE ( $\alpha$ S, SIGNAL SEQUENCE)  
 CGATAACCATGAAACTTCTTATCCTCACCTGTCTTGTGGCTGTTGCTCTTG  
 |  
 TATT — ETC.

$\alpha S_1$   hLZ SEQUENCE Bal II  
 —CCAAGGTCTTGAAGGTGTGAGTTGC  
 ETC.—AACC

FIG. 25.

APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

CONSTRUCTION OF 16.8 A hLZ3:

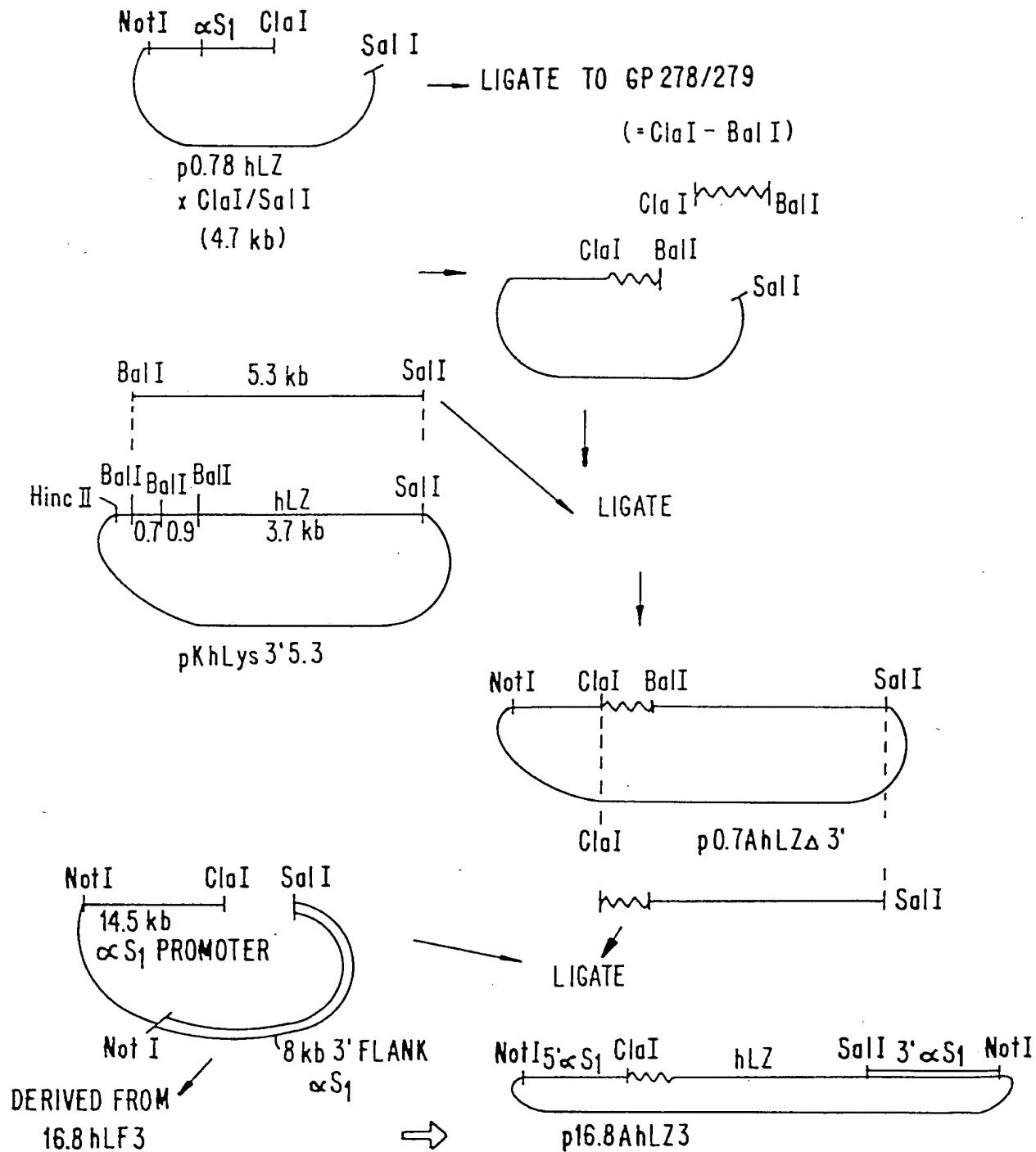


FIG. 26.

CONSTRUCTION OF 16A hLZ3:

APPROVED	O.G. FIG.
CLASS	SUBCLASS
BY DRAFTSMAN	

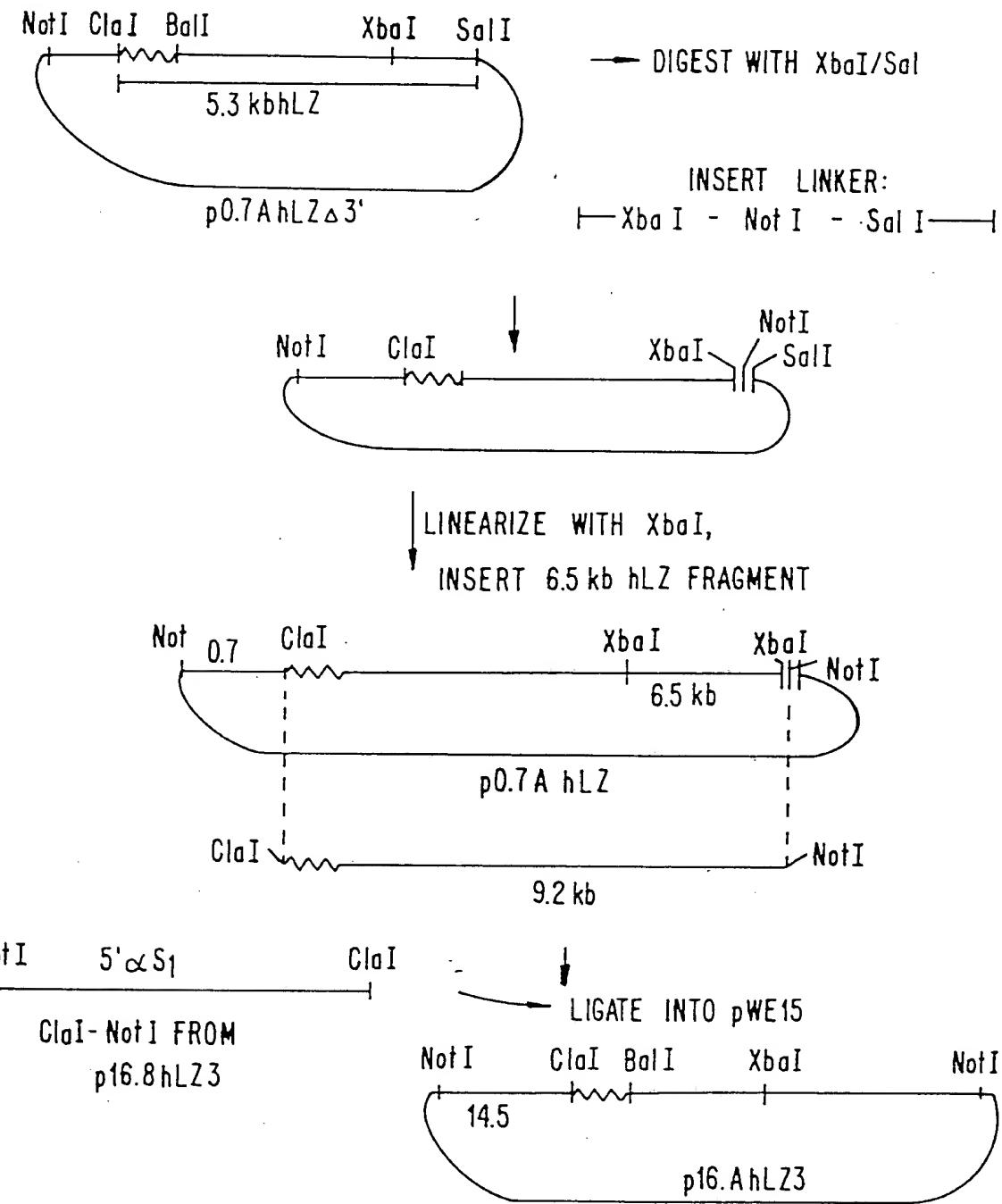


FIG. 27.